

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2002, 22:59:14 ; Search time 866 Seconds

(without alignments)
18626.341 Million cell updates/sec

Title: US-09-828-498-1

Perfect score: 9395

Sequence: 1 tgacgtgggggggtgatcc.....cccaagggcgggttctact 9395

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_032802.*
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2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA1983.DAT.*
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22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8100.6	86.2	9395	19	AAT76930
2	7979	84.9	9392	19	AAV66102
3	7979	84.9	9392	19	AAV56058
4	7979	84.9	9392	20	AAV16351
5	7979	84.9	9392	20	AAV02334
6	7979	84.9	9392	20	AAV82093
7	7977.4	84.9	9392	17	AAT08812
8	7971.8	84.9	9391	17	AAT15656
9	7971.8	84.9	9391	18	AAT94168

10	7885.6	83.9	9327	19	AAV66279
11	7885.6	83.9	9327	19	AAV56242
12	7885.6	83.9	9327	20	AAV16505
13	7885.6	83.9	9327	20	AAV02517
14	7885.6	83.9	9327	20	AAV82248
15	7884	83.9	9327	17	AAT08958
16	7760.6	82.6	9103	17	AAT15657
17	7760.6	82.6	9103	17	AAT08856
18	7760.6	82.6	9103	17	AAV66229
19	7760.6	82.6	9103	19	AAV56192
20	7760.6	82.6	9103	20	AAV16395
21	7760.6	82.6	9103	20	AAV02467
22	7760.6	82.6	9103	20	AAV82137
23	7548.2	80.3	9390	19	AAT76929
24	7548.2	80.3	9390	19	AAT76931
25	7469.6	79.5	9390	19	AAV23078
26	7418.6	78.9	9391	19	AAV23083
27	7414.4	78.9	9391	19	AAV23076
28	7373.8	78.5	9391	19	AAV23081
29	7373	78.5	9014	18	AAT45836
30	7369.6	78.4	9391	19	AAV23077
31	7311.6	77.8	9331	19	AAV23079
32	7288.2	77.6	9256	19	AAV23075
33	7243.6	77.1	9333	19	AAV23084
34	7200.8	76.6	9271	19	AAV23080
35	7141.6	76.0	9126	19	AAV39074
36	7141.2	76.0	9126	18	AAT96447
37	7141.2	76.0	9126	18	AAT45828
38	7106.6	75.6	9122	17	AAT42920
39	7034.6	74.9	9034	21	AAV55380
40	7033	74.9	9034	16	AAT04247
41	6711.8	71.4	8630	19	AAV23082
42	3861.8	41.1	5091	21	AAV55442
43	2143.4	22.8	2561	18	AAT94159
44	2141.8	22.8	2561	18	AAT94162
45	2141.8	22.8	2561	18	AAT94160

ALIGNMENTS

RESULT 1

AAT76930

ID AAT76930 standard; cDNA; 9395 BP.

AC AAT76930;

DT 11-SEP-1998 (first entry)

DE GT110 gene cDNA sequence for detection of GBV-C/HGV gene.

DE Hepatitis virus; GT230 gene; GT110 gene; GBV-C/HGV; detection; ss.

OS Hepatitis virus.

PN JP09276000-A.

PD 28-OCT-1997.

PF 18-APR-1996; 96JP-0134117.

PR 18-APR-1996; 96JP-0134117.

PA (NTAK-) NTAKKU YG.

DR WPI; 1998-022168/03.

PT NonA nonB non C hepatitis virus gene - used for the detection of

PT GBV-C/HGV in a sample

PS Claim 5; Pages 29-34; 42pp; Japanese.

CC This represents the cDNA sequence of the GT110 gene. Sequences shown in

Recombinant HGV se
HGV isolate 32HGV-
Polynucleotide seq
US5856134 Seq ID 2
Hepatitis G virus
Hepatitis G virus
HGV-JC variant pol
Hepatitis G virus
Hepatitis G virus
HGV variant JC cDN
Consensus sequence
US5856134 Seq ID 1
Hepatitis G virus
GT230 genomic RNA
cDNA se
Fragment HGJ1789 o
Fragment HGJ1737 o
Fragment HGJ1668 o
Hepatitis GB virus
Fragment HGJ1741 o
Fragment HGJ1916 o
Fragment HGJ606 of
Fragment FI029 of
Fragment HGJ2141 o
Hepatitis GB virus
Fragment of HGBV N
Hepatitis GB virus
GB-C viral genomic
Hepatitis GB virus
Hepatitis GB virus
Fragment HGJ1775 o
Hepatitis GB virus
Hepatitis G virus
Hepatitis G virus

Db 1981 TGTCGAAGCATTTAGTGGGGCTGGCCTTACGGGGGATTCTATGAACCCCTTGGTCGCA 2040
QY 2041 GGTGTTCCGAGCTGATGGAGCCGGAATCCGGTTTCCCGGGGTACGATGCTCTCCT 2100
Db 2041 GGTGTTCCGAGCTGATGGAGCCGGAATCCGGTCTGCCCCGGGTATGATGGCTTCCCT 2100
QY 2101 CTGTGTAGACCTACAGGGTTTCATACAGCTCCAGGGGACCTGACAGGAGTGGAATGGCGGA 2160
Db 2101 CGGGTCGGCTGATGGTTTATACATGTTACAGGACATTCGACGAGGTTGATGCAAGCA 2160
QY 2161 ACTTCATCCCTCCTCACAGCTGGTCTCTTGGATTTTGTATTTGCTCTATCTGA 2220
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QY 2221 TGAAGCTGGCTGAGGCACAGTTGGTCCCGTTGATCTTCTTCTGCTGCTGGTGGGTGA 2280
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QY 2281 ACCAGTTGGCGGTTCTAGGACTGCCGGCTGTGGACGCTGCCGTGGCGGGTGAAGTTTGTG 2340
Db 2281 ACCAGTTGGCGGTTCTAGGACTGCCGGCTGTGGACGCTGCCGTGGCGGGTGGTGGTGGTGA 2340
QY 2341 CGGGCCCTCCTCTGTCATGGTGTGGGCTTCCCACTGTCCACTGTCAATGATAGTACTAGTCTAG 2400
Db 2341 TGGGCCCGGCCCTGCTGCTGGTGTAGGCTTCCCACTGTCCCACTGTAGCATGATACCTGGTCTGG 2400
QY 2401 CAACCTGGTGTGTAATTTCCGTGGATGGCCCTCAGCGCCCTCATGTTCCCTGCTTGT 2460
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QY 2521 GGGCACTCTGTGTCGGGGCCGAGTCTCTGTCGATGTCACATTCGAGGTGGACACTT 2580
Db 2521 GGGCACTCTCGCTGTCGGGGCCGAGTCTCTGTCGATGTCACATTCGAGGTGGACACTT 2580
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Db 2581 CGGTGTTGGCTGGGTGGTGGCCAGTGTGGTGGCCATAGCGCTCCCTCAGCTCAA 2640
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Db 2641 TGAGCCAGGGGGTGGAGCAACAAGCCGTGATCTACAGAAGCTGTATAAGGGTACC 2700
QY 2701 AGGCTGTGGCCAGAGGGTGGTGGAGCCCTCGGGAGGGGGCTCTACCAAGCTTC 2760
Db 2701 AGGCTATTCCGCCAAGGGTGGTGGAGTCCCTCTCGGGAGGGGGCGCCAAACCAACCC 2760
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Db 2881 TGTGTTTCCGGGGCCCTCGTTCCGGCTTGTGGCGGGTGGTGGTGGTGGTGGTGGTGG 2940
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Db 3421 CCATCGCTACACCTGTGGGGCCCTAAATCCAGGTGGTGGTGGCAAGTGTGATGTC 3480
QY 3481 CGGTGTACCGCTTCCAGATGGGCAACTTTCGTTGAGCCCTGCACCTTGGCCAGCGGAGT 3540
Db 3481 CGGTGTACCGCTTCCCGGATGGGGCAACCTCTGTACACCTGCACCTTGGCCAGCGGAGT 3540
QY 3541 CTTGTTGGGTTATTAGATCCGACGGGCTTTGTGCCATGGCTTTGAGCAAGGGGCAAGG 3600
Db 3541 CTTGTTGGGTCATCCGATCAGACGGGCTTTATGCCATGGCTTTGAGCAAGGGGCAAGG 3600
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Db 3601 TAGAGCTGATGTGGCCATGAGGCTCTGATTTCCGTGGCTCTCTGTTGCTGCTGCTGCT 3660
QY 3661 TTTGCCACAAAGGACGACGATGAAGTCTGCTGTCAGTCTCAGTCTGCGGCGAGG 3720
Db 3661 TGTGTGACGAGGACGACGATGAGTCTGCTGTCAGTCTGCTGCTGCTGCTGCTGCTGCTG 3720
QY 3721 TTACTCGCGCGGATTCATCTAGCCGTGGACTCAAGTACCAACAGATGCGCAAGACTACCA 3780
Db 3721 TCACCGCGGCTCGATTCATCTAGCCGTGGACCCCAAGTTCCCAACAGATGCGCAAACTACCA 3780
QY 3781 CAGAACCCCTCGGTGGCGGCAAAAGGATTTTCAAGAGGCGCCGTGTTGTTATGCCTA 3840
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Db 3901 TAATCTTAAACCCCTCAGTGGCTACTGTGAGAGCCATGGGCCCTTACATGGAGCGACTG 3960
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Db 3961 CGGGGAAACATCAAGCATATCTGTGGCCATGACACCACTGCTTTTCACAGGATCACTG 4020
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Db 4081 GGGGGTTCGTTGGTCTATCTGTGACAGTGGCACAGCCATGACTCAACTGTGTGTGTTG 4140
QY 4141 GCATTTGGGCTGTACAGGAGCTGGCGGAGGATGTGGAGTGCAATTTGGTCTCTACGCCA 4200
Db 4141 GCATCGGGCGGTACGGGAGCTGGCGCGGCTGTGGAGTGCAGCTTGTGCTCTACGCCA 4200

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Qy	4261	ACGTGGGAGAGATCCCTTCTATGGCATGGCATACCTCTTTGACGGATCGGACCGGAA	4320
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Qy	4321	GGCATCTCGTATTTCTGCCACTCCAAGGCTGAGTGGAGCGCTGGCGGCGCAGTTTTCGG	4380
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Qy	4381	CTAGGGGGTAAATGCATCGCTATTACAGGGGAAAGACAGTTCTATCATCAAGATG	4440
Db	4381	CGAGGGGGTCAACGGCATCGCTATTATAGGGGAAAGACAGTTCTATCATCAAGACG	4440
Qy	4441	GAGACCTGGTGTGTGTGTACAGACGCATAATCCACTGGGTACACTGGGAACCTTCGATT	4500
Db	4441	GTGACCTGGTGTGTGTGCCACAGACGCATAATCCACCGGTACACTGGGAACCTTCGATT	4500
Qy	4501	CTGTACCCGATTTGGGTTAGTGGTGGAGAGGTCGTGAGGTGACCTTGATCCCCACCA	4560
Db	4501	CTGTCACTGATTTGGGTTAGTGGTGGAGAGGTCGTTGAGGTGACCTTGATCCCCACCA	4560
Qy	4561	TTACCATCTCCCTGGCAGAGTCCCGCGTGGCTGAACTGTGATGACGGCGGAGGAC	4620
Db	4561	TTACCATCTCCCTGGCAGAGTCCCTGCTGCGGCAAGAAATTTGCTGATGCAACGGCGAGGAC	4620
Qy	4621	GCAGGGTAGGGGACGTCGTGGGCGCTACTACTACGCGGGGTGCGGAAGCCCTCGCTG	4680
Db	4621	GCAGGGTAGAGGACGTCGTGACGCTACTACTACGAGGGGTGGGCAAGCCCTCGG	4680
Qy	4681	GTGTGTCGCTCAGTCTGCTGTGTCGGCGGTGGAAAGCCGCTGTGACCTGTGACGGAA	4740
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Qy	4741	TGGAACCTGACTTGACAGCAAACTACTGAGACTTTACGACACTGCCTTACACCGCAG	4800
Db	4741	CCGTGCGAGCTGACATTTGGGGAAGCCGGTGTCTTTTCGGGGCTTGCCTTGTGAGGA	4860
Qy	4801	CCGTGCGGGTGCATCTGGCGAGCGCGCTGTTTTTCTCCGGGCTTGCCTTGTGAGGA	4860
Db	4801	TGCATCCCGATGTAGCTGGGCAAAAGTCCGCGGCTCAATTTGCCCTCTTGTGTGGGTG	4920
Qy	4921	TTACAGCGACCATGTCCCGGGAAACACTGTCTCCCGGCCCATCGGATGACCCCGAGTGG	4980
Db	4921	TTACAGCGACCATGTCCCGGGAAACACTGTCTCCCGGTCCATTCGACGACCCCAATGGG	4980
Qy	4981	CAGTCTGAAGGCCCGAATCTCTGCCACTCCTCCTGAGTGGGGCAATGATTTACCAT	5040
Db	4981	CAGTCTGAAGGCCCGAATCTCTTCCACTACTCTCAGTGGTGGGCAATGATTTACCAT	5040
Qy	5041	CTAAGTGGCCGCCATACATCTGTGGAGCACTGTGTCCTAGCTCGGGTGC CGGAGG	5100
Db	5041	CTAAGTGGCCGCCACCACTTTGTGACGACTGTTTCGTAGCTCGTGTGGCGGAGG	5100
Qy	5101	GTTACGTCGCTCGGATGGGGACCCATCTTGTGTTGGGCTCGCTATTTGCGGGGGGCA	5160
Db	5101	GTTACGTCGCTCGGACGCGGGGCCCATCTTGTGTTGGGCTTGCCTATGACGAGGGGCA	5160
Qy	5161	TGATCTATGGCTCATACACGGGTCTCTCGTGGTGGTTACAGACTGGGATGTGAAGGGG	5220
Db	5161	TGATCTACGGGTCTTACACGGGTCTTGTGTTGGTGGTGCACAGACTGGGATGTGAAGGGG	5220
Qy	5221	GTGCGACCCCTTATCGGCATGAGACCGACGCCACGCCACCGCGTGTGCAAGTCC	5280
Db	5221	GTGCGACCCCTTATCGGCATGAGACCGACGCCACGCCACCGCGTGTGCAAGTCC	5280
Qy	5281	CCCCGTTAGACCATCGCGCGGGGGAGAGTCTGCGCCCATCGGATGCCAAACAGTGCAG	5340

Db	5281	CCCCCGTAGACCATTCCGCGGGGGGGAATCTGCGCCATCGGATGCCAAGACGTGACAG	5340
Qy	5341	ATGCGGTGGCGGCCATCCAGGTGGATTGCGGATTTGGTTCAGTCAATGACCCCTGTCATCGGG	5400
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Db	5401	AAATGCTGTCTTTAGCTCAGGCTTAAGACGGCGGAGCCCTACACAGCAACCGCAAGTGGC	5460
Qy	5461	TTTGTGGCTGTCTACAGGGGAGCGGGGCCGTCCCCACTGTTTCAATTGTTGACAACTCT	5520
Db	5461	TCGCTGGCTGTCTACAGGGGAGCGGGGCCGTCCCCACTGTTTCAATTGTTGACAACTCT	5520
Qy	5521	TCGCGGGGCTTGGCGGGCTGGTAGGCATTGCCACAGTGTAAATAGCTGCGGCAGTGG	5580
Db	5521	TTTGGCGAGGTTGGCTGCGTGGTGGGCCATTGCCACAGCTCATAGCTGCGCGCGTGG	5580
Qy	5581	CGGCTATGGGGCTTCTTAGGAGCCCTCCATTGGCTGCTGCCGCTTCCCTACCTCATGGGT	5640
Db	5581	CGGCTTACGGGGCTTCCAGAAGCCCGCGTTCGCGGCCGCGGCTTCCCTACCTCATGGGAT	5640
Qy	5641	TGGGCGTCCGAGGCAACGGCAACCCGCTTAGCCTCCGCTCTCCTACTAGGGGCCGCTG	5700
Db	5641	TGGGCGTCCGAGGTAACGGCAACGCGCTTGGCATCCGCTCTCCTATTGGGGCTGCTG	5700
Qy	5701	GGACGCTCTGGGCACGCTGCTGGTGGGTAAACCATGGCGGCGGTTTCATGGGAAGTG	5760
Db	5701	GTACGCGCTGGGCACGCTGCTGGGAGTAACCATGGCAGGTGGTTCATGGGGGGTG	5760
Qy	5761	CTAGGCTCTCCCTCTCTTGGTCACCAATTTACTGGGGCCGTGGGGGCTGGGAGGGCG	5820
Db	5761	CCAGCGTCTCCCTCTCTTGGTCACTATTCTACTAGGGCCGTGGGAGTTGGGAGGGCG	5820
Qy	5821	TGGTGAATGGGCTAGCCTTGTCTTCGACTTTATGGCGGGGAAACTATCATCAGAAGATC	5880
Db	5821	TTGTCAACCGGCAAGCCTTGCTTCGACTTTATGCGGGGAAGCTTTTCATCAGAAGATC	5880
Qy	5881	TCGTGTATGCCATCCAGTGCTAACCCAGTCCGGGGCAGGACTTCGGGGATCGCCCTCG	5940
Db	5881	TCGTGTATGCCATCCCGTGCTTAACCATGCTTGGGGGGGCGCTTCGGGGATCGCTCTTG	5940
Qy	5941	GGTGTGTGTGTACTCAGCTAACACTCTGGCACTACCCTTGGTTGAACCGTCTGCTGA	6000
Db	5941	GTCTGTTTGTACTCAGCTAACACTCTGGCACTACCCTTGGCTGAACCGTCTGCTGA	6000
Qy	6001	CTACATATGCCAAGTCTCATGCATCCCTGACAGTTTACTTTCAGCAGCGCGATTCATGTG	6060
Db	6001	CTACGTTGCGAGGTCTCGTGCAITTCCTGACAGCTTACTTCCAGCAGGCTGACTACTGCG	6060
Qy	6061	ACAAGTCTCAGTGTGCTCCGACGCTTCAGCCTCACTCGCACCGTGTTGCCCTGCTCA	6120
Db	6061	ACAAGTTTCGCGCGTGCTCCGCCGATTAGCGTGAACCGCACAGTGTGGCGCCTGGTCA	6120
Qy	6121	ACAGGAGGCTTAAGTGGATGAGTTACAGTGGGGTACGCTCGGAGCTTGTGGGAGTGGGA	6180
Db	6121	ACAGGAACCAAGTGGATGAGTGCAGGTGGGTACGCTCGGATCTCTGGGAGTGGGA	6180
Qy	6181	TCATCGCTCAAGTGCAGTGTGATGGCCAGACTTCGGGCCCTCTCGCCCGTGGTGTCAAT	6240
Db	6181	TCATCGCACAGTTGCGATGTTGTCATGGCCAGGCTCGGGGCCCTCTCGCCCGTGGTGTCA	6240
Qy	6241	TACCCCTATGGCACTCGCGGGAGGGTGTCCGGAGAAATGGTTGTGGAGCGCCATGTTG	6300
Db	6241	TCGCCCTGTGGCAATTCGCGGGAGGGTGTTCGCGGGAATGGCTGTGGAGCGTCAATGTTG	6300
Qy	6301	AGAGTCGTTGTCTTGTGGTTCGCTGATCACCGTGATGTTTGAATGGGCAACTCAAAG	6360
Db	6301	AGAGCGCTGTCTTGTGGATGTGTGATTAACCGGTGACGTTTTTGAATGGGCAACTCAAAG	6360
Qy	6361	ATCCAGTTTACTCTACCAAGCTGTGCAGGCATTTATGSGATGGGGACAGTCCCTGTGAACA	6420


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Qy 8581 CTTGGATCCTATACACACGGTGGGTATCATCCCTACGTGCTCACCCTGGCGGTTTAGG 8640
Db 8581 CTTGGATCCTATACACACGGTGGGTATCATCCCTACGTGCTCACCCTGGCGGTTTAGG 8640
Qy 8641 GTGGTGGACACACCTCTGATCCCTGTGGTCCAGGTACATGTAATTAATTAAGTTTC 8700
Db 8641 GTGGTGGACACACCTCTGATCCCGTATGGTCCAGGTGATGTAATTAATTAAGTTTC 8700
Qy 8701 CACTGGCAAACTGCCTAAATCATCTGTCGCTCCACGACACAGCGTTGAGGGTTA 8760
Db 8701 CACTGGCAAACTGCCTAAATCATCTGTCGCTCCACGACACAGCGTTGAGGGTTA 8760
Qy 8761 CCGCAGACAACTAAGCAAAATAGAGGTGTCGACAGGTGCTGAGGACCTCAAGTCC 8820
Db 8761 CCGCAGACAACTAAGCAAAATAGAGGTGTCGACAGGTGCTGAGGACCTCAAGTCC 8820
Qy 8821 CTGGCCTAGCAGTCCACCGGAGAGCGCGGGGATTTGCGAACCGCTATGCTCCGGTCG 8880
Db 8821 CTGGCCTAGCAGTCCACCGGAGAGCGCGGGGATTTGCGAACCGCTATGCTCCGGTCG 8880
Qy 8881 GCGGTTGGGCTGAGTTGGTAGGGGCTGTTGTGGCGTCCAGGCTCGGGCTTCCCGCTC 8940
Db 8881 GCGGTTGGGCTGAGTTGGTAGGGGCTGTTGTGGCGTCCAGGCTCGGGCTTCCCGCTC 8940
Qy 8941 CGGAGATTGCTGATCCCGGGGTTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCT 9000
Db 8941 CGGAGATTGCTGATCCCGGGGTTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCT 9000
Qy 9001 ATCAATTGGATTTCACAGCCAGAGAGTGCCTGGCGGTGGTGGGTTCTTAGCCCTGC 9060
Db 9001 ATCAATTGGATTTCACAGCCAGAGAGTGCCTGGCGGTGGTGGGTTCTTAGCCCTGC 9060
Qy 9061 TCATCTGAGCCCTCTCGGGTGAATTAATTCATCTCTTGGCGCAAGTCCGGTGAATGA 9120
Db 9061 TCATCTGAGCCCTCTCGGGTGAATTAATTCATCTCTTGGCGCAAGTCCGGTGAATGA 9120
Qy 9121 TCATCTGAGGAGGTTCGCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCT 9180
Db 9121 TCATCTGAGGAGGTTCGCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCTTCCCGCT 9180
Qy 9181 GCGCGGCTTGGAGGATGGTGTACTAAACCCCTTGGCAGGCTCAAGCCCTGATGGT 9240
Db 9181 GCGCGGCTTGGAGGATGGTGTACTAAACCCCTTGGCAGGCTCAAGCCCTGATGGT 9240
Qy 9241 GCTAATGACACTGACCTTCCGCTGCGGCTGCTACCTTATAGCGTAATCCGCTGACTACGG 9300
Db 9241 GCTAATGACACTGACCTTCCGCTGCGGCTGCTACCTTATAGCGTAATCCGCTGACTACGG 9300
Qy 9301 GCTGCTGACAGACCTTCCCGGATGGGACAGTGCATGTGATCTGAAGGGGTGCACC 9360
Db 9301 GCTGCTGACAGACCTTCCCGGATGGGACAGTGCATGTGATCTGAAGGGGTGCACC 9360
Qy 9361 CCGGTAAGAGCTCGGCAAGGCGGGTCTACT 9395
Db 9361 CCGGTAAGAGCTCGGCAAGGCGGGTCTACT 9395

RESULT 2
AAV66102
ID AAV66102 standard; cDNA; 9392 BP.
AC AAV66102;
AT
CT
DE HGV-PNF2161 variant cDNA sequence.
DE
KW PNF2161 sera; antigen; immunoreaction screening;
KW Non-A Non-B Non-C Non-D Non-E Hepatitis virus; HGV;
KW anti-HGV antibody; vaccine; ds.
XX
OS Hepatitis G virus.
XX
```

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FH Key Location/Qualifiers
FT CDS 459..9080
XX /*tag= a
XX
XX US5824507-A.
XX
XX 20-OCT-1998.
XX
XX 19-MAY-1995; 95US-0444733.
XX
XX 19-MAY-1995; 95US-0444733.
XX
XX 20-MAY-1994; 94US-0246985.
XX
XX 03-AUG-1994; 94US-0285543.
XX
XX 26-OCT-1994; 94US-0285561.
XX
XX 23-NOV-1994; 94US-0329729.
XX
XX 16-DEC-1994; 94US-0344271.
XX
XX 15-FEB-1995; 94US-0357509.
XX
XX 15-FEB-1995; 95US-0389886.
XX
XX (GENE-) GENELABS TECHNOLOGIES INC.
XX
XX Fry KE, Kim JP, Linnen JM, Wages J, Young LM;
XX
XX WPI; 1998-582553/49.
XX
XX P-PSDB; AAN80148.
XX
XX Polypeptide antigens hepatitis G virus - useful as vaccines against
XX the virus and raising antibodies for use in immuno-testing for the
XX virus
XX
XX Claim 10; Columns 99-118; 206pp; English.
XX
XX
XX The present sequence represents a Hepatitis G virus variant, isolated
XX from PNF2161 sera. This sera is obtained from a patient suffering from
XX Non-A Non-B Non-C Non-D Non-E Hepatitis Virus, also known as
XX Hepatitis G virus (HGV). HGV antigens can be identified from clones
XX isolated from PNF2161 sera. HGV antigens can be used in immunoreaction
XX screening for presence of anti-HGV specific antibodies, especially in
XX patient sera, e.g. enzyme linked immunoassay (ELISA). They can also be
XX used as vaccines, and to raise the polyclonal and monoclonal antibodies.
XX
XX
XX Sequence 9392 BP; 1694 A; 2551 C; 2998 G; 2148 T; 1 other;
XX
XX
XX Query Match 84.9%; Score 7979; DB 19; Length 9392;
XX Best Local Similarity 90.7%; Pred. No. 0;
XX Matches 8515; Conservative 1; Mismatches 876; Indels 1; Gaps 1;
XX
Qy 3 ACGTGGGGGGTTGATCCCCCCCCCGGCACGTGGGTGCAAGCCCAATAAACCCACGCCCT 62
Db 1 ACGTGGGGGGTTGATCCCCCCCCCGGCACGTGGGTGCAAGCCCAATAAACCCACGCCCT 60
Qy 63 ATCTAAGTAGACCAATGACTCGGCGCCGACTCGGCGACCGGCCCAAAAGGTGGTGGATGG 122
Db 61 ATCTAAGTAGACCAATGACTCGGCGCCGACTCGGCGACCGGCCCAAAAGGTGGTGGATGG 120
Qy 123 GTGGTGACAGGGTTGGTAGTCTGTAATCCCGGTTCATCTCGTAGCCACTATAGTGGGT 182
Db 121 GTGATGACAGGGTTGGTAGTCTGTAATCCCGGTTCATCTCGTAGCCACTATAGTGGGT 180
Qy 183 CTTAAGAGAAGGTCAAGACTCTCTTGTGCTTGGCGGAGACCGCCGACCGTCCACAGGT 242
Db 181 CTTAAGAGAAGGTCAAGACTCTCTTGTGCTTGGCGGAGACCGCCGACCGTCCACAGGT 240
Qy 243 GCTGGCCCTACCGGTGTAATAAGGGCCGACGTCAGGCTCGCTTAAACCGAGGCCGT 302
Db 241 GTTGGCCCTACCGGTGGAATAAGGGCCGACGTCAGGCTCGCTTAAACCGAGGCCGT 300
Qy 303 CACCCACCTGGCAACAGCAGCCACAGTCCAGTCCAGTCCGCTTCAATGTCTCTCTTG 362
Db 301 TACCCACCTGGCAACAGCAGCCACAGTCCAGTCCAGTCCGCTTCAATGTCTCTCTTG 360
Qy 363 ACCAATAGTCTTATCCCGCGAGTTGACAAGCAGTGGGGCGCGGGGTTATGGGAAG 422
Db 363 ACCAATAGTCTTATCCCGCGAGTTGACAAGCAGTGGGGCGCGGGGTTATGGGAAG 422
```


QY 2583 GTGTGGCTGGGTGGCGAGCGTGTGGCTTGGCCATAGCGCTCTGAGCTCAATG 2642
DB 2580 GTGTGGCTGGGTGGCGAGTGTGGTACGTTGGCCATTTGGCTCTGAGCTCGATG 2639
QY 2643 AGCGAGGGGGTGAAGCAAGCGGTGATCTATAGGAGGTGGTAAAGGTTACAG 2702
DB 2640 AGCGAGGGGGTGAAGCAAGCGGTGATCTATAGGAGGTGGTAAAGGTTACAG 2699
QY 2703 GCTGTGGCCAGAGGTGTGGCGAGCGCCCTCGGGAGGGCGCTCTACCAAGCTTCTG 2762
DB 2700 GCAATCCGCTAAAGGGTGGTGAAGAGCGCCCTCGGGAGGGCGCCCTGCGCAACCCCTG 2759
QY 2763 ACGTTCGCTGGCTTGGCCCTCATACATCTGGCCGATGCTGTGATGATGGTGGTG 2822
DB 2760 ACCTTGGCTGGCTTGGCCCTCATACATCTGGCCAGATGCTGTGATGATGGTGGTT 2819
QY 2823 GCCTTGGTCTCTTCGCGGCTGTTGCGACGACTGAGCTGGGCCCTCGGAGAGGCTCCTG 2882
DB 2820 GCCTTGGTCTCTTCGCGGCTGTTGCGACGCTTGGATGGGCTTGGAGGAGATCTTG 2879
QY 2883 GTCTCCGGCCCTCGTTACGGCGACTGCGAGGGTGGTGGAGTCTGTGATGGCGGGC 2942
DB 2880 GTGTCCCGGCGCTCGTTGCGCGGTTGGCTCGGGTGGTGGAGTCTGTGATGGCGGGT 2939
QY 2943 GAGAGGCCACCACTCCGACTGGTCTCCAAGATGTCCGAGAGGGGCGCTACTCTGTT 3002
DB 2940 GAGAGGCCACCACTCCGCGCTGGTCTCCAAGATGTGCGAGAGGAGCTTATTTGTT 2999
QY 3003 GACCACATGGGCTCTTCTCGCGGCTGTCAAGAGCGCTTGTGGAAATGGGAGCGGGCT 3062
DB 3000 GATCATATGGGCTCTTCTCGCGTGTCTCAAGAGCGGCTTGTGGAAATGGGAGCGAGCT 3059
QY 3063 TTGGAGCGCTGTCTATCTACGTAGGAGGAGTGTGCGCATCATCAGATGCGCGAGAGCC 3122
DB 3060 CTGGAACCTGTCTATCTACGTAGGAGGAGTGTGCGCATCATCAGGAGTGGCGAGGACT 3119
QY 3123 CTGTCTCGGACAGTGCCTCATGGGTTTACCGGTGTAGCAGCGCGGCTGTAGAGGTT 3182
DB 3120 TTGTCTCGGGGAGTGCCTCATGGTTTACCGGTGTGCGCGCGCTGTGTGATGAGGTT 3179
QY 3183 CTCATCGGCTCTTTCAGGATGTAATCATTTGGCTCCCGGGTTGTCCGACTGCACCA 3242
DB 3180 CTCATCGGCTCTTTCAGGATGTAATCATTTGGCTCCCGGGTTGTTCGAGCGCGGCT 3239
QY 3243 GTTGTCTATCCGCTGGGAAAGGGTTCCTGGGGGTTCAGAAAGGAGCGCTTGCACAGGT 3302
DB 3240 GTTGTCTATCCGAGCTGGGAAAGGGCTTCTTGGGGTTCACAAAGGCTGCCTTGACAGGT 3299
QY 3303 AGGATCTCTACTACATCCAGGAAGCTCATGTGTGGGAGCGGCTAGCTCAGAGC 3362
DB 3300 CGGATCTCTACTACATCCAGGAAGCTCATGTGTGGGAGCGGCTAGCTCAGAGC 3359
QY 3363 ATGGGCACATCTGTAATGGCTCTGTCTCAACTTTCCATGGGGTTCATCCCGAACC 3422
DB 3360 ATGGGAACATCTGTAAGGGCTCTGTCTCAGACCTTCCATGGGGTTCATCCCGAACC 3419
QY 3423 ATCCGACGCGGCTGGGGCGCTTAAATCCAGGTGGTGGTTCAGCAGTGTAGCTCAGC 3482
DB 3420 ATCCGACGCGGCTGGGGCGCTTAAATCCAGAGTGGTGGTTCAGCAGTGTAGCTCAGC 3479
QY 3483 GTGTACCGGCTTCAGATGGGGCAACTTCGTGTAGCGGCTTCGACTTGGCAGGGAGTCC 3542
DB 3480 GTGTATCCACTCCCGGATGGGGCTTACTTCGTTAAACACTTGTACTTGCAGGGCTGATCC 3539
QY 3543 TGTGGGTATTAGATCCGAGGGGCTTGTGGCATGCTGTGACAAAGGGGACAAAGGTT 3602
DB 3540 TGTGGGTTCATCAGATCCGAGGGGCGCTATGCCATGGCTTGTGACAAAGGGGACAAAGGTT 3599
QY 3603 GAGCTGATGGGCATGGAGGCTCTGACTTCGCTGGTGTGCTGTGTTTACCGGCTCCTT 3662
DB 3600 GAGCTGATGGGCATGGAGGCTCTGACTTCGCTGGCTGCTGCTCAGCGTCCCTA 3659
QY 3663 TGGACAAAGGGCAGGAGTAAGAAATGCTGTGTCACTGTCTCCACTCTGGGGGAGGAGTT 3722

DB 3660 TGTGACGAAGGCGACGAGTAGGAATGCTGTGTCTGTCTCCTCCTCGGTGTAGGGTC 3719
QY 3723 ACTGGCGCGGATTTACTAGGCGGTGGACTCAAGTACCAACAGATGCCAAGACTACACA 3782
DB 3720 ACCGCGCAGCGGTTCATAGGCGGTGGACCAAGTGCACAGATGCCAAGACTACTACT 3779
QY 3783 GAACCCCTCCGTTGGCGGCAAGAGGATTTCAAGAGAGCGCGGTTGTTTATGCCCTACG 3842
DB 3780 GAACCCCTCCGTTGGCGGCAAGAGGATTTCAAGAGAGCGCGGTTGTTTATGCCCTACG 3839
QY 3843 GGGCGGGAAGAGCACCCGCTACCTTGGAGTACCGGCACACATGGGCCCAACAGGCTTG 3902
DB 3840 GGAGCGGGAAGAGCACCTCGCTCCCGCTTGGAGTACGATTAACATGGGCGCAAGGCTCTTA 3899
QY 3903 ATCTTGAACCCGCTGGTAGTACCGTGAAGGCCATGGGCCCATACATGGAGCGGCTGGCG 3962
DB 3900 ATCTTGAACCCCTCAGTGGCCACTGTGCGGCCATGGGCCCATACATGGAGCGGCTGGCG 3959
QY 3963 GGAACACACCCAGTATTTACTGTGGCCATGACACCACTGCTTTCAAGGATCACTGAC 4022
DB 3960 GTTAACATCCAAGTATATCTGTGGCATGATACACTGCTTTCAAGGATCACTGAC 4019
QY 4023 TCGCCCTTACGATTTCCACTTACGGAAGGTTTTTGGCCAAACCTTAGGCAGATGCTGAGG 4082
DB 4020 TCCGCCCTGAGCTATTTCAACCTATGGGAGCTTTTGGCCAAACCTTAGGCAGATGCTACGG 4079
QY 4083 GGTGTGCTGGTGTCTATTTGTGAGGAGTGGCGGAGGATGTGGAGTGAATTTGGTCTACGCCACT 4202
DB 4080 GGCCTTTCGTTGCTATTTGTGATGATGTCACAGTCACTCAACCTGCTGTTTAGGC 4139
QY 4143 ATTGGGCGTCTAGGAGCTGGCGGAGGATGTGGAGTGAATTTGGTCTCTACGCCACT 4202
DB 4140 ATTGGGAGATCCGGAGCTGGCGGCTGGGTGGGGTGGCACTAGTCTCTACGCCACC 4199
QY 4203 GCCACCCCTCCCGATCCCGATGCCAGTACCCAGCACCCATCAATCATTTAGACAAAACCTGGAC 4262
DB 4200 GCTACACCTCCCGATCCCGATGATGACGACGACCCCTTCCCATATTTAGACAAAATTTGGAC 4259
QY 4263 GTGGGAGATCCCTCTATGGCATGGCATACCTCTTCAGCGGATGGCGACCGGAAGG 4322
DB 4260 GTGGCGAGATCCCTTTTATGGCATGGAAATACCCCTCGAGCGGATGGCAACCGGAAGG 4319
QY 4323 CATCTCGTATTTGCCACTCCAAGGCTGAGTGGAGCGCTGGCGGCCAGTTTTCGGCT 4382
DB 4320 CACCTCGTGTCTGCCATTTCTAAGGCTGAGTGGAGCGCTTGTGCGCCAGTTTCTCGCT 4379
QY 4383 AGGGGGTAAATGCCATCGCTATTACAGGGGGAAGACAGATTTCTATCATCAAGATGGA 4442
DB 4380 AGGGGGTCAATGCCATTCCTATTATAGGGGTAAGACAGATTTCTATCATCAAGGATGGG 4439
QY 4443 GACCTGTGTGTGTGTACAGACGCACTATCCACTGGGTACACTGGGAACCTTCGATTCCT 4502
DB 4440 GACCTGTGTGTGTGTGTACAGACGCGCTTTCCTACTGGGTACACTGGAAATTTTCGACTCC 4499
QY 4503 GTCAACGATTTGGGTGAGTGGAGGAGTGTGTGAGTGGAGGCTTGTATCCACCACT 4562
DB 4500 GTCACCGACTGTGATTTAGTGGTGGAGGAGTGTGTGAGTGGAGGCTTGTATCCACCACT 4559
QY 4563 ACCATCTCCCTGCGCAGGTTGCCCGCTCGGCTCAACTGTGATGCGAGCGGCGGAGGACGC 4622
DB 4560 ACCATCTCCCTGCGCAGGTTGCCCGCTCGGCTGAACTGTGATGCGAAGACGAGGACGC 4619
QY 4623 ACCGGTAGGGGAGGCTGGGCGCTACTACTACGCGGGGCTGGCAAGGCGGCTGCTGCT 4682
DB 4620 ACCGGTAGGGGAGGCTGGAGCGCTACTACTACGCGGGGCTGGCAAGGCGGCTGCGGCT 4679
QY 4683 GTGTGCGCTCAGGCTCTGTCTGTGTGCGGCTGGAAGCGGCTGTGACTGTGATCGGAATG 4742
DB 4680 GTGTGCGCTCAGGCTCTGTCTGTGTGCGGCTGGAAGCTGGAGTGGAGTGTGACTGTGATCGGAATG 4739
QY 4743 GAACCTGACCTGACAGCAAAACCTACTCAGACTTTACGACAACTGCCCTTACCGCGAGCC 4802

Db 4740 GAACCTGACTTGACAGCTAACCTACTGAGACTTTACGAGACTGCCCTTACACCCGAGCC 4799
QY 4803 GTCGACGCTGACATTCGGGAAGCCGGGTGTTCTTTTCGGGGCTTCGCCGCTTGAGGATG 4862
Db 4800 GTCGGGCTGATATCGGAGAGCCGGGTGTTCTCTCGGGCTCGCCCATTTGAGGATG 4859
QY 4863 CATCCGCTGTTAGCTGGGCAAAAGTTCGCGGCTCAACTGGCCCTTCCTGTTGGGTGTT 4922
Db 4860 CACCCGTGATGTAGCTGGGCAAAAGTTCGCGGCTCAACTGGCCCTTCCTGTTGGGTGTT 4919
QY 4923 CAGCGACCATGTGCGGGGAACACTGTCTCCGGGCCATCGGATGACCCAGTGGGCA 4982
Db 4920 CAGCGACCATGTCTCGGGGAACACTGTCTCCGGGCCATCGGATGACCCCAATGGGCA 4979
QY 4983 GGTCTGAAGGGCCGCAATCTGTGCCACTCTCTGCTGAGTGGGCAATGATTTACCATCT 5042
Db 4980 GGTCTGAAGGGCCCAATCTGTCTCCACTCTCTGCTGAGTGGGCAATGATTTACCATCT 5039
QY 5043 AAGTGGCCGGCCATCACATCTGTGGACGACCTGGTCCCTAGGCTCGGGGTGGCGGAGGT 5102
Db 5040 AAGTGGCCGGCCACCATAGTGGACGACCTGGTCCCGGAGACTCGGCTGGCGGAGGT 5099
QY 5103 TAGCTCCGCTGGATGCGGGGACCATCTTGATGGTGGGCTCGCTATTGGGGGGGCATG 5162
Db 5100 TAGCTCCGCTGGACCTGGGGGATCTTGATGATCGGCTAGCTATCGCGGGGGAATG 5159
QY 5163 ATCTATGCTGATACACCGGGTCTCTGTTGGTGTACAGACTGGGATGGAAGGGGT 5222
Db 5160 ATCTAGCGGTATACACCGGGTCTCTGTTGGTGTACAGACTGGGATGGAAGGGGT 5219
QY 5223 GCGAGCCCTTTATCGGCATGAGACAGGCGCACCCAGCCGCTGTGTCAGGTCCCC 5282
Db 5220 GCGCCCTCTTTATCGGCATGAGACAGGCGCACCCAGCCGCTGTGTCAGGTCCCT 5279
QY 5283 CCGGTAGACCATCGCGGGGAGAGTCTGCGCCATCGGATGCGCAACAGTGCAGAT 5342
Db 5280 CCGGTAGACCATCGCGGGGGTGAATCAGCACCATCGGATGCCAAGACAGTGCAGAT 5339
QY 5343 GCGGTGGCGCCATCAGGTGATTCGATGTCAGTGCATGACCTGTCGATCGGGAA 5402
Db 5340 GCGGTGGCAGCCATCAGGTGATTCGATGTCAGTGCATGACCTGTCGATCGGGAA 5399
QY 5403 GTGCTGCTTGGCCAGGCTAAGACGGCGGAGGCTACGAGCTACCCAGTGGCTT 5462
Db 5400 GTGTTGCTTGGCTCAGGCTAAGACGGCGGAGGCTACACAGCAACCCAGTGGCTC 5459
QY 5463 GCTGGCTGTACACGGGAGCGGGCGCTCCCACTGTTTCAATGTTGACAGCTCTTC 5522
Db 5460 GCTGGCTGTATACGGGAGCGGGCGCTTCCCACTGTATCCATTTGTCACAGCTCTTC 5519
QY 5523 GCGGGGGCTGGCGGCTGTGTAGCCATGCGCAGTGTATAGCTGGCGAGTGGCG 5582
Db 5520 GCGGAGGTGGCGGCTGTGTGGGCCATGCGCAGCGTGTATGCTGGCGGTGGCG 5579
QY 5583 GCTATGGGCTTCTAGGAGCCCTTCATTTGGTGTCTGCGCTTCCCTACCTCATGGGTTG 5642
Db 5580 GCTACGGGCTTCAAGAGCCCGCTTGGCAGCGCGCTTCCCTACCTCATGGGTTG 5639
QY 5643 GGGGTGGAGGCAACCGCAACCCGCTTAGCTTCGCTCTCTACTAGGGCCGCTGGG 5702
Db 5640 GGGTTTGGAGGAACGCTCAGAGCGCCCTGGGCTCTGCGCTCTCTATTGGGGCTGTGGA 5699
QY 5703 ACGGCTGCGGACGCTCTGTTGGGTTAAACATGCGGGGCGCTTACATGGAGTGTCT 5762
Db 5700 ACGGCTTGGGCACTCTGTGTGGGCTTGACCATGGCAGGTGCTCATGGGGGGGGCC 5759
QY 5763 ACGGCTCCCGCTTCTTGGTACCATTTTACTGGGGCGCTGGGGGCTGGAGGGCGTG 5822
Db 5760 AGTGTCTCCCGCTTGTGTACCATTTTATGGGGCGCTCGAGGTTGGGAGGTGTT 5819
QY 5823 GTGAATGCGGCTAGCCTTCTCTGACTTTATGGCGGGGAAACTATCATCAGAAGATCTG 5882
Db 5820 GTCAACGCGGAGGCTAGTCTTTGACTTTATGCTGATGGCGGGGAAACTTTTCATCAGAAGATCTG 5879

QY 5883 TGGTATGCCATCCAGTGTCTAACCACTCGGGGGCAGGACTTTCGGGGATCGCCCTCGG 5942
Db 5880 TGGTATGCCATCCGCTACTGACCACCGCGGGGGCGGCTTCGCGGGATCGCTCTCGG 5939
QY 5943 TTGGTGTCTACTACAGTAACTCTGCGACTTACACTTGGTTGAACCGTCTGCTGACT 6002
Db 5940 TTGGTGTCTATTCAGCTAACTCTGCGACTTACACTTGGTTGAACCGTCTGCTGACT 5999
QY 6003 ACATTCGCAAGTCTCTATGCATCCCTGACAGTTACTTTTCAGCAGGCGGATTTACTGTAC 6062
Db 6000 ACGTTACCAAGTCTTCTATGATCCCGGACAGTTACTTTTCAGCAAGTTGACTATTGCGAC 6059
QY 6063 AAGGCTCTAGCTGTCTCCGAGCGTTGAGCTCACCTCGCACCGCTGTGCGCTTGGTCAAC 6122
Db 6060 AAGGCTCTAGCGCTGTCTCCGGCGCTGAGCTCACCGGCACAGCTGTGCGCTTGGTCAAC 6119
QY 6123 AAGGAGCTTAAGTGTGATGAGTTTTCAGTGGGTAGCTCTGGGACTTGTGGGAGTGGATC 6182
Db 6120 AAGGAGCTTAAGTGTGATGAGTTTTCAGTGGGTAGCTCTGGGAGCTGTGGGAGTGGATC 6179
QY 6183 ATGCGCTCAAGTGGCATGTGATGGCCAGACTTCGCGGCGCTCTGCCCGTGGTGTCTATTA 6242
Db 6180 ATGCGCAAGTGGCTGTGTCATGGCCAGACTCAGGGCGCTCTGCCCGTGGTGTCTACATA 6239
QY 6243 CCCTTATGCACTTCGCGGAGGGGTGTCGCGAGAAATGTTTGTGGACGGCCATGTTGAG 6302
Db 6240 CCCTTGTGCATTCGCGGAGGGGTGTCGCGGAAATGTTTGTGGACGGCTCATGTTGAG 6299
QY 6303 AGTCGCTGTCTTGTGGTTCGCTGATCACCGGTGATGTTTGAATGGCAACTCAAGAT 6362
Db 6300 AGTCGCTGTCTTGTGGTTCGCTGATCACCTGTTGACGTTCTGTAATGGCAACTCAAGAA 6359
QY 6363 CCAGTTTACTCTACCAAGCTGTGACGCAATTTTGAATGGGAGACAGTCCCTGTGAACATG 6422
Db 6360 CCAGTTTACTCTACCAAGCTGTGCGGCACTATTGATGGGAGCTGTCCCTGTGAACATG 6419
QY 6423 GTGGGCTATGGCGAGAGCTGCGCTTTCGCTCAGACACACCCGAGGTGGTACCATTC 6482
Db 6420 GTGGGTTAGGTGAACAGTTCGCTCTCGGCTCGACACACCCGAGGTGGTGGCCCTTC 6479
QY 6483 GGGACCTCTGGTGGCTGAGTGGTGGTACCCCTACCCACGTTGTGATCAGCGGAACA 6542
Db 6480 GGGACCTCTGGTGGCTGAGTGGTGGTGGTACCCCTACCCACGTTGTGATCAGAGGACC 6539
QY 6543 TCGGCTTACAACTGCTGGCCAGCAAACTCTGCGCTGCTGCTGAGCCCTATTAC 6602
Db 6540 TCGGCTTAAAGCTGCTGGCCAGCAAACTCTATCGGCTGCTGAGCTGAGCCCTACTAC 6599
QY 6603 GTCGAGCGCATACCGGCTCTATGGGACGCGGACGCGGCTGCCATGGTCTATGGC 6662
Db 6600 GTCGAGCGCATTCGCTCTATGGGACGCGGACGCTGTCGCGCCCGCTATGGCTATGGC 6659
QY 6663 CCTGGCAAAAGTGTACCATTTGACGGGAACTACACCCCTCCCGCATCAACTGCGGCTT 6722
Db 6660 CCTGGCAAAAGTGTACCATTTGACGGGAGGCTACACCTTGGCTCATCAACTGAGGCTC 6719
QY 6723 AGGAATGGGCGGCTCTGAGGTGTCTATGGGAGTGTCAATTTGACATTTGGGAGGAGACT 6782
Db 6720 AGGAATGGGCGGCTCTGAGGTTCATCCGAGGTGTCCATTTGACATTTGGGAGGAGACT 6779
QY 6783 GAAGACTCAGAACTGACTGAGGCGGCTGCGCGCGGCGCTGACGCTTTCAGGCTATC 6842
Db 6780 GAAGACTCAGAACTGACTGAGGCGGCTGCGCGCGGCGGCTGCTGCTTCCCAAGGATC 6839
QY 6843 GAGAATGCTCGGAGAACTTCTTGAACCTCACATAGATGTCTATCATGGAAGATTTGAGTACA 6902
Db 6840 GAGAATGCTCGGAGGATTTCTTGAACCGCACATTTGATGTCTATCATGAGGAGTTCAGTACA 6899
QY 6903 CCCTCTCTTTTGGGAGTACCGGAGAGTCCCTGCTGTTGGGAGAGACATACCCCCCACT 6962
Db 6900 CCCTCTCTTTTGGTGTAGTACCGGAGAGTCCCTGTATGGGAGAGACATACCCCCCACT 6959

Db 9120 ATCACCGGAGGAGTTCCCGCCCTCCCGCCCGCCAGGGGTCTCCCGCTGGGTAAAGGG 9179

Qy 9183 CCCGCCCTTGGGAGCATGGTGTACTAAACCCCTGGCAGGGTCAAAAGCCTGATGGTGC 9242

Db 9180 CCCGCCCTTGGGAGCATGGTGTACTAAACCCCTGGCAGGGTCAAAAGCCTGATGGTGC 9239

Qy 9243 TAATGCACTGCCACTTCCGGTGGCGGGTCCGTACCTTTATAGCGTAATCCGTGACTACGGGC 9302

Db 9240 TAATGCACTGCCACTTCCGGTGGCGGGTCCGTACCTTTATAGCGTAATCCGTGACTACGGGC 9299

Qy 9303 TGCTCGCAGAGCCCTCCCGGATGGGCACAGTGCATGTGATCTGAAGGGGTGCACCCC 9362

Db 9300 TGCTCGCAGAGCCCTCCCGGATGGGCACAGTGCATGTGATCTGAAGGGGTGCACCCC 9359

Qy 9363 GGTAAAGCTCGGCCCAAGGCCGGGTCTACT 9395

Db 9360 GGGAGAGCTCGGCCCAAGGCCGGGTCTACT 9392

RESULT 3

AAV56058

ID AAV56058 standard; cDNA: 9392 BP.

AC AAV56058;

XX 06-NOV-1998 (first entry)

XX HGv isolate PNF 2161 variant cDNA.

XX Immunoreactive; detection; antibody; alanine aminotransferase;

KW Non-A, Non-B, Non-C, Non-D, Non-E hepatitis virus; ds.

XX Hepatitis G virus.

XX Key Location/Qualifiers

FT CDS 459..9080

FT /*tag= a

XX US5766840-A.

XX 16-JUN-1998.

XX 05-JUN-1995; 95US-0466033.

XX 19-MAY-1995; 95US-0444733.

XX 20-MAY-1994; 94US-0246985.

XX 03-AUG-1994; 94US-0285543.

XX 03-AUG-1994; 94US-0285558.

XX 03-AUG-1994; 94US-0285561.

XX 26-OCT-1994; 94US-0329729.

XX 23-NOV-1994; 94US-0344271.

XX 16-DEC-1994; 94US-0357509.

XX 15-FEB-1995; 95US-0389886.

XX 05-JUN-1995; 95US-0466033.

XX (GENE-) GENELABS TECHNOLOGIES INC.

XX Fry KE, Kim JP, Linnen JM, Wages J, Young LM;

PI WPI; 1998-361677/31.

XX P-PSDB; AAW76054.

XX Antibody to hepatitis G virus protein - useful for diagnosis of

PT hepatitis G virus infection

XX Example 13; Column 99-120; 204pp; English.

XX This sequence is a used in a method which detects Non-A, Non-B, Non-C,

CC Non-E hepatitis G virus (HGV) in a biological fluid sample, e.g.

CC from a test subject, especially using a kit comprising an anti-HGV

CC antibody preparation and a reporter for detecting binding of an HGV

CC polypeptide antigen to the antibody, preferably where the antibody is

CC monoclonal and/or is attached to a solid support and where the reporter

CC is a labelled monoclonal antibody or a labelled competing antigen. The

CC HGV is characterised by producing elevated serum alanine aminotransferase

CC levels in an infected primate, being serologically distinct from

CC hepatitis A, B, C, D and E viruses and having a viral genome containing a

CC nucleic acid region that is selectively hybridisable with a polypeptide

CC having 203 base pairs as given in the specification.

XX

SQ Sequence 9392 BP; 1694 A; 2551 C; 2998 G; 2148 T; 1 other;

Query Match 84.9%; Score 7979; DB 19; Length 9392;

Best Local Similarity 90.7%; Pred. No. 0;

Matches 8515; Conservative 1; Mismatches 876; Indels 1; Gaps 1;

Qy 3 ACGTGGGGGGTTGATCCCGCCCGCCCGCTGGGTCAAGCCCATATAACCGACGGCT 62

Db 1 ACGTGGGGGGTTGATCCCGCCCGCCCGCTGGGTCAAGCCCGCCCGACGCGCT 60

Qy 63 ATCTAAGTAGAGCAATGACTGGCGCGGACTGCGGACCGGCCCAAAAGGTGGATGG 122

Db 61 ATCTAAGTAGAGCAATGACTGGCGCGGACTGCGGACCGGCCCAAAAGGTGGATGG 120

Qy 123 GTGGTGACAGGGTTGGTAGGTGCTAAATCCCGGTCTATCTGGTAGCCACTAGGTGGGT 182

Db 121 GTGGTGACAGGGTTGGTAGGTGCTAAATCCCGGTCTATCTGGTAGCCACTAGGTGGGT 180

Qy 183 CTTAAGAGAAGGTCAAGACTCTCTTGTGCTTGCCTGCGCGGAGACCGCGCACAGGT 242

Db 181 CTTAAGAGAAGGTCAAGACTCTCTTGTGCTTGCCTGCGCGGAGACCGCGCACAGGT 240

Qy 243 GCTGCCCTACCGGTGTGAATAAGGGCCCGACGTGAGGTCTGTCTTAAACGAGCCCGT 302

Db 241 GTTGGCCCTACCGGTGGGAATAAGGGCCCGACGTGAGGTCTGTCTTAAACGAGCCCGT 300

Qy 303 CACCACCTGGGCAACGACGCGGACGTACGGTCCACGTGCGCCCTTCAATGTCTCTTG 362

Db 301 TACCACCTGGGCAACGACGCGGACGTACGGTCCACGTGCGCCCTTCAATGTCTCTTG 360

Qy 363 ACCAATAGGTTTATCCGGCGAGTTGACAAGGACCAAGTGGGGCCGGGGTATGGGAAG 422

Db 361 ACCAATAGGTTAGCGCGGAGTTGACAAGGACCAAGTGGGGCCGGGGCT-TGAGAGG 419

Qy 423 GACCCCAACCCCTGCCCTTCCCGGTGGCGGGAATGCATGGGGCCACCCAGCTCCGG 482

Db 420 GACTCCAAAGTCCCGCCCTTCCCGGTGGCGGGAATGCATGGGGCCACCCAGCTCCGG 479

Qy 483 CGGGCTCGACCGGGGTAGCCCAAGAATCTTCGGGTGAGGGCGGGTGGCAATTTCTTT 542

Db 480 CGGGCTCGACCGGGGTAGCCCAAGAATCTTCGGGTGAGGGCGGGTGGCAATTTCTTT 539

Qy 543 TTCTATACCATCATGGCAGTCTCTTCTGCTCTCTTCGCTTTCGCTTTCGCTTTCGCT 602

Db 540 TTCTATACCATCATGGCAGTCTCTTCTGCTCTCTTCGCTTTCGCTTTCGCTTTCG 599

Qy 603 GCGCGGCCACCCAGCTTGTGAGCGAATGGCAATATTCCTCACAAATTCGTGTGTC 662

Db 600 GCGCGGCCACCCAGCTTGTGAGCGAATGGCAATATTCCTCACAAATTCGTGTGTC 659

Qy 663 CCGGAAGACATCGGGTCTGCTGCGGAGCGGATCCCTGGTGGCCCTGGGGTGCACGGT 722

Db 660 CCGGAAGACATCGGGTCTGCTGCGGAGCGGATCCCTGGTGGCCCTGGGGTGCACGGT 719

Qy 723 TCCACCGACCGTTGCTGGCCACTGTATCAGCGGGGTTTGGCTGTGCGGCTGGCAAGTCC 782

Db 720 TCCACTGACCAATGCTGGCCACTGTATCAGCGGGGTTTGGCTGTGCGGCTGGCAAGTCC 779

Qy 783 GCGGCCACAGCTGTTGGGGAACCTGGGAGCCCTGTACGGGCCCTTTCGCTCTCGGCTTAC 842

Db 780 GCGGCCCAACTGGTGGGAGCTGGGTAGCCCTATACGGGCCCTTTCGCTCTCGGCTTAC 839

Qy 843 GTAGCCGGATCTGGGTCTGGGCGAGTTTACTCCGGGGTCTTACAGTTGGTTCGG 902

Db 840 GTGGCTGGGATCTGGGCTGGGTGAGGTGTACTACGGGTGTCCTAACGGTGGGAGTCGG 899

QY 903 TTGAGGCGCGGTCTACCTGATGCCAACCTGAAGTGTGCAGTAGAATGTGACGTTAAG 962
DB 900 TTGACGCGCGGTCTACCGCGTGCCTAACCTGACGTGTGCAGTGCAGTCTAAG 959
QY 963 TGGGGAAGTGAAGTTTGGAGATGGAGTGAAGTGGCCCTCAATTTACTTGGATTTGGAA 1022
DB 960 TGGGAAAGTGAAGTTTGGAGATGGAGTGAAGTGGCCCTCAATTTACTTGGATTTGGAA 1019
QY 1023 TACCTTTGAAAGTCCCATTTGAATTTTGGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1082
DB 1020 TACCTCTGAAAGTCCCATTTGAATTTTGGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1079
QY 1083 GTTGGGTGGCCCATTTGCTTTTGGAGCAACAGGATTTGATGATGATTTTCTGCTGGTG 1142
DB 1080 GTTGGGTGGCCCATTTGCTTTTGGAGCAACAGGATTTGATGATGATTTTCTGCTGGTG 1139
QY 1143 ACATGGCGGGGATTTGCAAGCGCCCGCTTCCGTTTGGGTTCGCGCCCTTTGAC 1202
DB 1140 ACATGGCGGGGATTTGCAAGCGCCCGCTTCCGTTTGGGTTCGCGCCCTTTGAC 1199
QY 1203 TACGGTTGAAGTGGCAGTCACTCTCTGAGGGCTAACGGGTTCGCGTATTTCCACTGGG 1262
DB 1200 TACGGTTGACTTTGGCAGACCTGCTTTGAGGGCCCAACGGTTTCGCTTTTTCAGTGGG 1259
QY 1263 GAGAGGTGTGGGATCGAGGGAATGTCAGCTCTTGTGTGACTGCCCCAACGGCCCTTGG 1322
DB 1260 GAGAAGTGTGGGACCGTGGGAAGTTACGCTTTCAGTGTGACTGCCCCAACGGCCCTTGG 1319
QY 1323 GTTGGGTCCCGGCTTTTCCAGGCGGTTGGTGGGGGACCCCATACCCATTTGGAGC 1382
DB 1320 GTGTGTTGACACCTTTTGGCAAGCAATCGGCTGGGGTGACCCCATCACTTAATTGGAGC 1379
QY 1383 CACGGACAAACAGTGGCCCTTATCATGCCCCCAATATGCTATGGGTCTGTGTCGGTA 1442
DB 1380 CACGGGCAAAATCAGTGGCCCTTTTATGCCCCCAAGTATGCTATGGGTCTGTACAGTC 1439
QY 1443 ACGTGCGTGTGGGTTCCGTTCTTGGTTTGCCTCGACCGCGGTCGTGATTCGAAGATC 1502
DB 1440 ACTTGGTGTGGGTTCCGTTCTTGGTTTGCCTCCACCAAGTGTGCGGACTCGAAGATA 1499
QY 1503 GATGTGTGGAGTTTGTGCGCGGTTGATCTGCCAGTGCACCATGACCGCTCTAGGTC 1562
DB 1500 GATGTGTGGAGTTTGTGCGCGGTTGATCTGCCAGTGCACCATGACCGCTCTAGGTC 1559
QY 1563 TCGGATCGCACACGTTGAGTCTCCGAGTGGGGAGTCCCGTCCGTAAGCTGATT 1622
DB 1560 TCGGATCGCACACGTTGAGTCTCCGAGTGGGATCCCGTCCGTAAGCTGATT 1619
QY 1623 CTGGACCGTGGGCTGCTTCATGTGGCACTGTGTGCGGAGTGTGTGCGGACCTGTCG 1682
DB 1620 CTGGACCGTGGGCTGCTTCCTGCGGCACCTGTGTGAGGAGTGTGTGCGGACCTGTC 1679
QY 1683 TCGGTTAGATTCCTTTCCATTCGGTGGGACCGGGGCTCGGCTGACAAAGGACTTGGAA 1742
DB 1680 TCGGTTAGATTCCTTTCCATTCGGTGGGAGTGGGGCTCGGCTGACAAAGGACTTGGAA 1739
QY 1743 GCTGTGCTCTGCTGCAACAGCAACTCCCTTCACCAATAAGGGCCCTTGGGCAACAG 1802
DB 1740 GCTGTGCTCTGCTGCAACAGCAACTCCCTTCACCAATAAGGGCCCTTGGGCAACAG 1799
QY 1803 GGGAGAGCAACCGGTGCGGTCGCGCTTGGGTTTGGGTCCTACACCATGACCAAGATC 1862
DB 1800 GGGAGAGCAACCGGTGCGGTCGCGCTTGGGTTTGGGTCCTACACCATGACCAAGATC 1859
QY 1863 CGGATTCCTTCGATTTGGTGAATTTCCACACACCGCATAGAGCCTCCGACTGGNACG 1922
DB 1860 CGAGATACCTTACATCTGTTGGTGAATTTCCACACACCGCATAGAGCCTCCGACTGGNACG 1919
QY 1923 TCCGGTCTTCCCGGAGTCCCGCCATTTAAACACTGATCGCGTGTAGGACGGAAGTG 1982
DB 1920 TTTGGGTTCTTCCCGGAGCGCCCTCTCAACAACTGATGCTCTTGGGACGGAAGTG 1979
QY 1983 TCTGAGGCATTTGGCGGAGCTGGGCTTACGGGGGGGTTCTACGAGCCTCTGTTTCGAGG 2042

DB 1980 TCCGAGGACATTTGGGGGGCTGGCCCTCACGGGGGGTTCATGAACCCCTGGTGGCGAGG 2039
QY 2043 TGTTCGGAGCTGATGGGACCGCGAAATCCGGTTTCCCGGGGTACGCATGGCTGTCTCT 2102
DB 2040 TGTTCGAAGCTGATGGGAGCGCGAAATCCGGTTTGTCCGGGGTTTGCATGGCTCTCTCG 2099
QY 2103 GGTAGACCTGACGGGTTTCATACACGTCCAGGGGACCTGCGAGAGGTGGATCGCGGCAAC 2162
DB 2100 GGCAGGCTGATGGGTTTATACATGCCAGGTCATTTGCAGAGGTGGATCGAGCAAC 2159
QY 2163 TTTATCCCTCCCTCCACGCTGGTGTCTTGGATTTGTATTTGTCTCTCTATCTGATG 2222
DB 2160 TTTATCCCGCCCGCGCTGGTGTCTTGGACTTTGTAATTTGTCTCTTATACCTGATG 2219
QY 2223 AAGCTGGCTGAGGCAAGGTTTGTCTCCGTTGATCTTCTCTCTCTGCTGTGGGTGAAC 2282
DB 2220 AAGCTGGCTGAGGCAAGGTTTGTCTCCGCTGATCTTCTCTCTGCTGTGGGTGAAC 2279
QY 2283 CAGTTGGCGGTTCTAGGACTGCCGGCTGTGGAGCTGCCGTGGCGGGTCAAGTTTGGG 2342
DB 2280 CAGCTGGCAGTCTAGGGCTGCCGGCTGTGGAAGCGCGCTGGCAGGTGAGTCTTCGGG 2339
QY 2343 GGCCTGCTCTGATGTTTGGGCTTCCACTGTCAGTATGATAGTGTCTAGCA 2402
DB 2340 GGCCTGCTCTGATGTTTGGGCTTCCGCTGTCAGTATGATAGTGTGGTGGCA 2399
QY 2403 AACCTGGTGTGATTTTCGGTGGATGGGCTTACGCGCTCATGTTCTCTGTTGTGG 2462
DB 2400 AACCTGGTGTGATTTTCGGTGGATGGGCTTACGCGCTCATGTTCTCTGTTGTGG 2459
QY 2463 AAGCTGCTGCGGGAGCTTTCCGCTGGGCACTTTTGTATGGGATTTTCGGGACCGCGGG 2522
DB 2460 AAGCTGCTGCGGGAGCTTTCCGCTGGGCTTCTTGTATGGGATTTTCGGGACCGCGGG 2519
QY 2523 CGCACCTGCTGCTCGGGCGGAGTCTCTCGATGTCACATTCAGGTGGACACTTCG 2582
DB 2520 CGCACCTGATGCTCGGGCGGAGTCTCTCGATGTCACATTCAGGTGGACACTTCG 2579
QY 2583 GTGTTGGGCTGGTGTGGCCAGCGTGGTGGCTTGGGCCATAGCGCTCTGAGCTCAATG 2642
DB 2580 GTGTTGGGCTGGTGTGGCCAGTGGTAGCTTGGGCCATTCGCTCTGAGCTCGATG 2639
QY 2643 AGCGAGGGGGTGGAAAGCACAGGCGGTGATCTATAGGACCTGGTGTAAAGGTTACCAG 2702
DB 2640 AGCGAGGGGGTGGAGGACAAAGCGGTGATCTATAGGACCTGGTGTAAAGGTTACCAG 2699
QY 2703 GCTGTGGCGCAGAGGCTGTGGGAGCGCCCTCGGGAGGGCGCTCTACCAAGCTTCTG 2762
DB 2700 GCAATCCGTCAAAGGTTGGTGAAGAGCCCTCGGGAGGGCGGCTGCCAAACCCCTG 2759
QY 2763 ACCTTCGCTGTGCTTGGCCTCATACATCTGGCCGATGCTGTGATGATGGTGGTGG 2822
DB 2760 ACCTTCGCTGTGCTTGGCCTCATACATCTGGCCAGATGCTGTGATGATGGTGGTGG 2819
QY 2823 GCCTTGGTCTCTCTTCGCGCTGTTCGAGCAGTGTGAGTGGCCCTTGGAGGAGCTCTG 2882
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QY 2883 GTCTCCGGCCCTCGTTACGGCGACTGGGACGCTGTTGAGTGTGATGGCGGGC 2942
DB 2880 GTCTCCGGCCCTCGTTGCGGCTTGGGCTGAGTGTGATGGCGGGT 2939
QY 2943 GAGAAGGCCACCACTCCGACTTCCCAAGATGTGCGCAAGAGGGGCTTACCTGTGTT 3002
DB 2940 GAGAAGGCCACCACTCCGCTTCCCAAGATGTGTCGAGAGAGGCTTATTTGTTTC 2999
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DB 3000 GATCATATGGGCTCTCTTTTCGCGCTGTTCAGAGGCGCTTGTGGAATGGGACGAGCT 3059
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Db 3120 TTGTCTCTGGGACAGTGCCTGATGGGTTTACCCTGGTAGCAGCGCGGTGATGAGGTT 3179
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Db 3240 GTTGTATCCGTCAGGTCGGAAAGGCTTCTTGGGGTACAGAGGCCTCCCTTGACAGT 3299
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Db 3300 CGGGATCCTGACTTACATCCAGGGAACGTCATGGTGTGGGACGGCTACGTCGGGAACG 3359
QY 3363 ATGGGACATGTCTGAATGGCCTGCTGTTCACAACTTTCCATGGGGCTTCATCCCGAACG 3422
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QY 3483 GTGTACCCGCTTCCAGATGGGCAACTTCTGTGACGCCCTGCACCTTGCCAGCGGAGTCC 3542
Db 3480 GTGTATCCACTCCGATCGGGTACTTCTGTTAAACCTTGTACTTGGCCAGGCTGAGTCC 3539
QY 3543 TGTGGGTTTATTAGATCCGACGGGGCTTGTGCCATGGCTTGAGCAAGGGGACAAAGGTT 3602
Db 3540 TGTGGGTTTATCAGATCCGACGGGGCTTATGCCATGGCTTGAGCAAGGGGACAAAGGTT 3599
QY 3603 GAGCTGGATGTGGCCATGAGGTCTGTGACTTCCGTGGTTCGTGGTTCACCGTCTCT 3662
Db 3600 GAGCTGGATGTGGCCATGAGGTCTGTGACTTCCGTGGTTCGTGGTTCACCGTCTCTA 3659
QY 3663 TGCAGAAAGGGCACGACGTAAGATGCTCGTGTGACGTCTCCACTCTGGCGGACAGGTT 3722
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QY 3723 ACTGGGCGGATTCATAGGCGGTGGATCAAGTACCAACAGATGCCAAGACTACCA 3782
Db 3720 ACCGGGCAAGGTTCACTAGGCGGTGGACCAAGTGCCAACAGATGCCAAGGCTACT 3779
QY 3783 GAACCCCTCCGTCGCGGCAAGAGGTTTCAAGAGGCGCCGCTGTTTATGCTAGC 3842
Db 3780 GAACCCCTCCGTCGCGGCAAGAGGTTTCAAGAGGCGCCGCTGTTTATGCTAGC 3839
QY 3843 GGGGGGAAAGACACCGCGTACCCTTGGAGTACGGCAACATGGGCGCACAGGTTCTTG 3902
Db 3840 GGAGCGGAAAGACACCTCCGCTGGAGTACGATAACATGGGCGACAAAGGTTCTTA 3899
QY 3903 ATCTGAACCGCTGGTACTACCTAGGCGGATGGGCGGATACATGAGGCGGTGGCG 3962
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QY 3963 GGAACACCCAGATTTTACTGTGGCCATGACACCACTGCTTTCACAAAGGATCACTGAC 4022
Db 3960 GGTAAACATCCAAAGTATATCTGTGGCATGTATCAACTGCTTTTCAAGAGTCACTGAC 4019
QY 4023 TCGCCCTTACGTTATTCACGTAAGGTTTGGCCAAACCTTAGGCGAGTGTGAGG 4082
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QY 4263 GTGGAGAGATCCCTTCTATGGGATGACATACCTCTTTGAGCGGATGGGACCGGAAGG 4322
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QY 4563 ACCATCTCCTCGGACGCTGCCGCTCGGCTGAACTGTGATGACGCGGAGGACG 4622
Db 4560 ACCATCTCCTCGGACAGTGTGCTGCTGGTGAAGTGTGACCTGATGCAAGACGAGGACG 4619
QY 4623 ACGGTTAGGGGAGGCTCTGGGCGCTACTACTACGCGGGGTGGCAAGCCCTCTGCTGT 4682
Db 4620 ACGGTTAGGGGAGGCTCTGGGCGCTACTACTACGCGGGGTGGCAAGCCCTCTGCTGT 4679
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QY 4743 GAACCTGACTGACAGCAAACTTACTGAGACTTTACGACAACCTGCCCTTACACCGCAGCC 4802
Db 4740 GAACCTGACTTGCAGCTAACTACTGAGACTTTACGAGACTGCCCTTACACCGCAGCC 4799
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Db 4980 GGTCTGAAGGGCGGCAATCTGTCCCACTCTCTGCTGAGTGGGCGAATGATTTACCATCT 5039
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QY 5103 TACGTCGCTGATGCGGGACCCATCTTTGATGTTGGGCTCTGCTATTCGCGGGGCGATG 5162
Db 5100 TACGTCGCTGATGCGGGACCCATCTTTGATGATGATGATGATGATGATGATGATGATGATG 5159
QY 5163 ATCTATGCTGATACACCGGCTCTCTGTTGGTGTGTACAGACTGGGATGTGAAGGGGTT 5222
Db 5160 ATCTAGCGCTGATACACCGGCTCTGTTGGTGTGTACAGACTGGGATGTGAAGGGGTT 5219
QY 5223 GCGAGCCCTTTATCGGCATGGAGACGAGCCACCGCCAGCCGCTGTGAGGTTCCCG 5282
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Db 7500 GTTACCANTCCAGCAATGTGGACGAGGGTGGACAAGGTGACCTTCTGGCGTGTCTCT 7559
QY 7563 AGGGTTTCATGACAAATTCCTCTGGSACTCCATAGAGCGCGCTAAGAGGCGAGCTCAAGCC 7622
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Db 7860 CCCCCCTGGACTTCGGGATGCTGAAAAGCTTATTCTGGGAGACCTCGACGGGTAGCC 7919
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Db 7980 ATGCTCAAACTGGAATCAAGAGAGACCCCTTGGGCCATCTGTGGAGCGCACCTGC 8039
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Db 8160 ACCCCGAGGGGTGCCAGTGGGTGAGAGTATTGTAGATCCCTCAGGGGTCTTGACCACC 8219
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QY 8763 GCAGACACAACCTAAGCAAAAAATGAGGCTGGCAAGGTGCTGAGCGACCTCAAGCTCCCT 8822
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Db 8820 GGCTTAGCAGTCCACCGGAAGAGCGCGGCGTTTGGCAACACGATGCTCCGCTCGCGC 8879
QY 8883 GGTGGGCTGAGTGGCTAGGGGCTGTTGTGGCTCCAGGCGCTGCGGCTTCCCTCCG 8942
Db 8880 GGTGGGCTGAGTGGCTAGGGCTTGTGTGGCATCCAGGCGCTACGGCTTCCCTCCCT 8939
QY 8943 GAGATTGCTGGTATCCCCCGGGGTTTCCCCCTTTCCCCCTTATATGGGGTGGTTCAT 9002
Db 8940 GAGATTGCTGGTATCCCCCGGGGTTTCCCCCTTCTCTCCCCCTTATATGGGGTGGTACAT 8999
QY 9003 CAATTGGATTTCACAAGCAGAGAGTGGCTGGCGGTGGTGGGGTCTTAGCCCTGCTC 9062
Db 9000 CAATTGGATTTCACAAGCAGAGAGTGGCTGGCGGTGGTGGGGTCTTAGCCCTGCTC 9059
QY 9063 ATCGTAGCCCTTCGSGTGAATTAATCATCTGTGGGCAAGTTCGCGTCACTGATC 9122
Db 9060 ATCGTAGCCCTTCGSGTGAATTAATCATCTGTGGGCAAGTTCGCGTCACTGATC 9119
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Db 9120 ATCACTTGGAGAGGTTCCCGCTCCCGCCCGCAGGGGTCTCCCCCTGGGTAAAAAGGG 9179
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Db 9180 CCGGCTTGGGAGGATGGTGTACTAACCCCTTGGCAGGCTCAAGGCTGATGGTC 9239
QY 9243 TAATGCACTGCCACTTCCGTGGCGGTGCTACCTTATAGCTAATCCGCTACGGC 9302
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QY 9303 TGCTCGCAGAGCCCTCCCGGATGGGCGACAGTGCATCTGTGATCTGAAGGGGTGACCCC 9362
Db 9300 TGCTCGCAGAGCCCTCCCGGATGGGCGACAGTGCATCTGTGATCTGAAGGGGTGACCCC 9359
QY 9363 GGTAAAGAGTCCGCCCAAGGCGGGTTCTACT 9395
Db 9360 GGTAAAGAGTCCGCCCAAGGCGGGTTCTACT 9392

RESULT 4
AA16351
ID AA16351 standard; cDNA; 9392 BP.
XX
AC AA16351;
XX
DT 22-JUL-1999 (first entry)
XX
XX Polynucleotide sequence of HGV-PNF 2161 variant.
XX
XX Hepatitis G virus; HGV; HGV-E2 antigen; vaccine; viral replication;
KW treatment; HGV infection; antisense; ds.
XX
XX Hepatitis G virus.
OS
XX

PN US5874563-A.
XX
PD 23-FEB-1999.
XX
PF 05-JUN-1995; 95US-0485910.
XX
PR 19-MAY-1995; 95US-0444733.
PR 20-MAY-1994; 94US-0246985.
PR 03-AUG-1994; 94US-0285543.
PR 03-AUG-1994; 94US-0285558.
PR 26-OCT-1994; 94US-0329729.
PR 23-NOV-1994; 94US-0344271.
PR 16-DEC-1994; 94US-0357509.
PR 15-FEB-1995; 95US-0389886.
PR 05-JUN-1995; 95US-0485910.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fry KE, Kim JP, Linnen JM, Wages J, Young LM;
XX
DR WPI: 1999-180067/15.
DR P-PSDB; AA94511.
XX
PT Isolated polynucleotide sequences derived from the Hepatitis G Virus
PT that encode the E2 antigen - useful for producing vaccines and
PT inhibitors against Hepatitis G, and for assays to detect the virus
PT in a sample
XX
PS Claim 1; Column 97-118; 206pp; English.
XX
CC The specification describes isolated polynucleotide sequences, derived
CC from a Non-A, Non-B, Non-C, Non-D, Non-E (N-ABCD E) Hepatitis Virus
CC (designated Hepatitis G or HGV). HGV is characterized by stimulating
CC production of serum alanine aminotransferase in primates infected with
CC the virus, being serologically distinct from the Hepatitis A, B, C, D
CC and E viruses, and being a member of the Flaviviridae virus family.
CC The HGV-E2 antigens, encoded by the polynucleotide sequences of the
CC invention, may be produced by standard recombinant DNA techniques,
CC and used in the preparation of vaccines. Anti-sense oligonucleotides
CC (and oligonucleotide analogues which encode portions of the sequences
CC disclosed in the specification) may be used to prevent expression of
CC the HGV-E2 genes by blocking transcription and preventing them
CC functioning normally in viral replication. Antisense sequences may be
CC used in this way as part of a treatment strategy against HGV infection.
CC The single stranded nature of the viral genome makes HGV highly
CC susceptible to inhibition in this way. The present sequence represents
CC the polynucleotide sequence of HGV-PNF 2161 variant.
XX
SQ Sequence 9392 BP; 1694 A; 2551 C; 2998 G; 2148 T; 1 other;
Query Match 84.9%; Score 7979; DB 20; Length 9392;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 8515; Conservative 1; Mismatches 876; Indels 1; Gaps 1;
QY 3 ACGTGGGGGGTGTATCCCCCCCCCCCGGCACTGGGTGCAAGCCCAATAAACCGACGCT 62
DB 1 ACGTGGGGGGTGTATCCCCCCCCCCCGGCACTGGGTGCAAGCCCAATAAACCGACGCT 60
QY 63 ATCTAAGTAGAGCAATGACTCGGCGCCGCACTCGCGGACCGCCAAAGGTGGTGGATGG 122
DB 61 ATCTAAGTAGAGCAATGACTCGGCGCCGCACTCGCGGACCGCCAAAGGTGGTGGATGG 120
QY 123 GTGGTGACAGGGTGTGGTAGTCCGTAATCCCGGTGATCTGGTAGCCACTATAGTGGGT 182
DB 121 GTGATGACAGGGTGTGGTAGTCCGTAATCCCGGTGATCTGGTAGCCACTATAGTGGGT 180
QY 183 CTTAAGAGAAGGTCAAGACTTCCTTTGTGCGCGGAGACCGCGCACGGTTCACAGT 242
DB 181 CTTAAGAGAAGGTCAAGACTTCCTTTGTGCGCGGAGACCGCGCACGGTTCACAGT 240
QY 243 GCTGGCCCTACCGGTGTGAATAAGGCGCGGAGTCAAGTCAAGTCAAGTCAAGTCAAGT 302
DB 241 GTTGGCCCTTACCGGTGTGAATAAGGCGCGGAGTCAAGTCAAGTCAAGTCAAGTCAAGT 300

QY 303 CACCCACCTGGGCAAAACGACGCCACGTTACGTTCCACGTCGCCCTTCAATGTCTCTCTTG 362
DB 301 TACCCACCTGGGCAAAACGACGCCACGTTACGTTCCACGTCGCCCTTCAATGTCTCTCTTG 360
QY 363 ACCAATAGTGTATCCCGCGAGTTTGACAAGACCAAGTGGGGGCCGGGGTGTATGGGGAAG 422
DB 361 ACCAATAGTGTATCCCGCGAGTTTGACAAGACCAAGTGGGGGCCGGGGTGTATGGGGAAG 419
QY 423 GACCCCAAAACCTTCCCTTCCCGTGGCGCGGGAATGATGGGGCCACCCAGCTCCCGG 482
DB 420 GACTCCAAGTCCCGCCCTTCCCGTGGCGCGGGAATGATGGGGCCACCCAGCTCCCGG 479
QY 483 CGGCTCGACGCGGGGTAGCCCAAGAAATCTTCGGGTGAGGGGGTGGCAATTTCTCTT 542
DB 480 CGGCTCGACGCGGGGTAGCCCAAGAAATCTTCGGGTGAGGGGGTGGCAATTTCTCTT 539
QY 543 TTCTATACCATGCGAGTCTTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 602
DB 540 TTCTATACCATGCGAGTCTTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 599
QY 603 GCGCGGCCACCCAGCTTGTGAGCGGAATGGGCAATATTTCTCTCACAATTTGCTGTGCC 662
DB 600 GCGCGGCCACCCAGCTTGTGAGCGGAATGGGCAATATTTCTCTCACAATTTGCTGTGCC 659
QY 663 CCGGAAGACATCGGTTCTGCTGCTGGAAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
DB 660 CCGGAGGACATCGGTTCTGCTGCTGAGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 719
QY 723 TGCACCGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 782
DB 720 TGCACCGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 779
QY 783 GCGCGGCCAGCTTGTGGAAGCTGGGAGCTGTACGGGCGCTTGTGCTGCTGCTGCTGCTGCT 842
DB 780 GCGCGGCCAATCGTGGGGAGCTGGGTAGCTATACGGGCGCTGCTGCTGCTGCTGCTGCTGCT 839
QY 843 GTAGCGGGGCTCGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 902
DB 840 GTGCTGGGATCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 899
QY 903 TTGAGGCGCCGGGTCTACCTGATGCCCACTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 962
DB 900 TTGAGCGCGCGGCTACCGGCTGCTAACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 959
QY 963 TGGGGAAGTGTGAGTGTGAGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1022
DB 960 TGGGGAAGTGTGAGTGTGAGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1019
QY 1023 TACCTTTGGAAAGTCCCATTTTGAATTTTGGAGAGGAGTGTGAGCTGAGCTGAGCTGAGCTG 1082
DB 1020 TACCTCTGGAAGTCCCATTTTGAATTTTGGAGAGGCTGTGAGCTGAGCTGAGCTGAGCTG 1079
QY 1083 GTTGGGTGGCGCATTCCTTTGCTGGAGCAACGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1142
DB 1080 GTTTCGCTGGCGCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1139
QY 1143 ACGATGGCGGGATGCTGCAAGGCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1202
DB 1140 ACGATGGCGGGATGCTGCAAGGCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1199
QY 1203 TACGGGTTGAAGTGCAGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1262
DB 1200 TACGGGTTGACTTGCAGACCTGCTTCTTTCAGGGGCAACGCTGCTGCTGCTGCTGCTGCTG 1259
QY 1263 GAGAGGTGTGGGATCGAGGGAATGTACGCTCTTGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1322
DB 1260 GAGAAGGTGTGGGACCTGTTACCGTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 1319
QY 1323 GTTGGGTGCCCGCTTTTGCAGCGGCTGGGTGGGGGACCCCATCACCATTTGGAGC 1382
DB 1320 GTGTGGTTGCCACGCTTTTGGCAAGCAATCGGCTGGGGTGAGCCCATCACATTTATGGAGC 1379

QY 1383 CACGACAAACAGTGGCCCTATCATGCCCCCAATATGTCTATGGTCTGTGCCGTA 1442
Db 1380 CACGGCAAAATCAGTGGCCCTTTTCATGCCCCAGTAGTGTCTATGGTCTCTACAGTC 1439
QY 1443 ACGTGGGTGGGGTTCGGTGTCTTGGTTTGGCTCGACGGGGTCTGTGATTCGAAGATC 1502
Db 1440 ACTTGGGTGGGGTTCGGTGTCTTGGTTTGGCTCCACAGTGGTGGGACTCSAAGATA 1499
QY 1503 GATGTGTGAGTGTGGTGGCCGTGGATCTGCCAGTGCACCATAGCCGCTCTAGGGTCA 1562
Db 1500 GATGTGTGAGTGTAGTGCCAGTTGGCTGTGCCACTGCACCATAGCCGACTTGGATCA 1559
QY 1563 TCGGATCGGACACGGTGGTGTGAGTCTCCGAGTGGGGAGTCCCGTGGGTAACTGTAAT 1622
Db 1560 TCGGATCGGACACGGTGGTGTGGCTTCCGAGTGGGGAATCCCGTGGGTGACGTGTGT 1619
QY 1623 CTGGACGTCGCGCTCTCATGTGCGCACTCTGTGCGGGACTGCTGCCCCAAACCGGG 1682
Db 1620 CTGGACGTCGCGCTCTCTCGCGCACTCTGTGAGGGACTGCTGGCCCGAGACCGGG 1679
QY 1683 TCGGTTAGATTCCTTTCATCGGTCCGCAACGGGCTCGGCTGACAAAGACTTGGAA 1742
Db 1680 TCGGTTAGGTTCCCATTCATCGGTGGCGTGGGCTCGGCTGACAAAGACTTGGAA 1739
QY 1743 GCTGTGCCCTTCGTCACAGGACAACTCCCTTCACATAAAGGGGCCCTGGGCAACAG 1802
Db 1740 GCTGTGCCCTTCGTCACAGGACAACTCCCTTCACATTTAGGGGCCCTGGGCAACAG 1799
QY 1803 GGGAGGCAACCGGTGGGTTCGCGCTCGGCTTGGTTCCTACACATGACCAAGATC 1862
Db 1800 GGGAGGCAACCGGTGGGTTCGCGCTCGGCTTGGTTCCTACGCACTGACCAAGATC 1859
QY 1863 CGGGATTCCTCATTTGGTGAATGTCCACACAGGCATAGAGCTCCGACTGGAAG 1922
Db 1860 CAGATACCTACATCTGGTGAAGTGTCCACACAGCCATAGAGCTCCACCGGAGG 1919
QY 1923 TTTGGGTTCTTCCCGGAGTCCCGCCATTAACAACTGCATCCGCTAGGCAAGGATG 1982
Db 1920 TTTGGGTTCTTCCCGGAGCGCGCTCTCAACAACTGCATCTTTGGGCAAGGATG 1979
QY 1983 TCTGAGGCAATTTGGGCGAGCTGGGCTTACGGGGGGTCTACGAGCCCTGTTCGCAGG 2042
Db 1980 TCCGAGGCAATTTGGGCGGCTGGGCTTACGGGGGGTCTATGAACCCCTGTTCGCAGG 2039
QY 2043 TGTTCGGAGCTGATGGGACCGGAAATCCGGTTTCCCGGGGTACGCATGGCTGTCTCT 2102
Db 2040 TGTTGGAAGCTGATGGGAAGCGAAATCCGGTTTTCGGGGTTTGCATGGCTCTCTCG 2099
QY 2103 GGTAGACCTGACGGTTTCATACACGTCCAGGGGCACTGCAGGAGTGGATCGGGCAAC 2162
Db 2100 GGCAGGCTGATGGTTTATACATGTCCAGGGTCACTTGCAGGAGTGGATGCAGGCAAC 2159
QY 2163 TFCATCCCTCTCCAGCTGGTGTCTTGGATTTTGTATTTGTCTGTCTATCTGATG 2222
Db 2160 TFCATCCCGCCCTCGCTGGTGTCTTGGACTTTGTATTTGTCTGTCTATACCTGATG 2219
QY 2223 AAGCTGGCTGAGGCAAGTGGTGGCTGTGATCTTGTCTGTCTGTGGTGGTGAAC 2282
Db 2220 AAGCTGGCTGAGGCAAGTGGTGGCTGTGATCTTGTCTGTCTGTGGTGGTGAAC 2279
QY 2283 CAGTTGGGGTTCTAGGACTCGCGCTGTGGACGCTGGCGTGGCGGGTGAAGTTTTCGG 2342
Db 2280 CAGCTGGCAGTCTAGGCTCGCGCTGTGGAAGCGCGCTGGCAGGTGAGTCTTCGG 2339
QY 2343 GGCCTCGCTTCATGTTGGTGTGGGCTTCCCACTGTCAGTATGATAGTCTAGCA 2402
Db 2340 GGCCTCGCTTCCTGTGTCTGGGACTTCCCGGCTGTCAGTATGATATTGGGTTTGGCA 2399
QY 2403 AACCTGGTGTCTACTTTCGGTGGATGGGCTCTCAGGCTCATGTCCTCGTGTGG 2462
Db 2400 AACCTGGTGTCTACTTTAGATGGTGGGACCCCAAGCCCTGATGTCCTCGTGTGG 2459
QY 2463 AAGCTCGCTCGGGAGCTTTCCCGCTGGCACTTTTGTATGGGATTTTCGGCGACCCGCGG 2522

Db 2460 AAGCTTGTCTCGGGAGCTTTCCTCGCTGGCCCTTGTATGGGATTTTCGGCGACCCGCGG 2519
QY 2523 CCACTCTGTCTCTCGGGCCAGTTCGTCTCGATGTACATTCGAGGTGACACTTCG 2582
Db 2520 CCACTCTCAGTCTCTCGGGCCAGTTCGTCTCGATGTACATTCGAGGTGACACTTCG 2579
QY 2583 GTGTGGGCTGGTGGCCAGCGTGTGGCTTGGCCATAGCGCTCTCGAGCTCAATG 2642
Db 2580 GTGTGGGCTGGTGGCCAGTGTGTAGCTTGGCCATTCGCTCTCGAGCTCGATG 2639
QY 2643 ACGGAGGGGGTGGAAACAAAGCCGTGTATCTATAGACGTGTGTAAAGGTACACAG 2702
Db 2640 ACGGAGGGGGTGGAGGCAAAAGCCGTGTATCTATAGACGTGTGTAAAGGTACACAG 2699
QY 2703 GCTGTGCCCAAGAGGTGTGGGAGCCCTCGGGAGGGGCTCTCTACCAAGCTCTG 2762
Db 2700 GCAATCCGTCAAAAGGTGTGTAGGAGCCCTCGGGAGGGGCGCTGCCAAACCCCTG 2759
QY 2763 ACGTTCGCTGTGTGGCTTCATACATCTGCCCGGATGCTGTGTATGATGTTGGTGTG 2822
Db 2760 ACGTTCGCTGTGTGGCTTCATCTCTGCCAGATGCTGTGTATGATGTTGGTGTG 2819
QY 2823 GCTTTGGTCTCTCTTGGGCTGTTCGACGCACTGGGCTTGGGCTTGGAGGAGTCTCTG 2882
Db 2820 GCTTTGGTCTCTCTTGGGCTGTTCGACGCGTGTGGATTTGGGCTTGGAGGAGATCTCTG 2879
QY 2883 GTCTCCCGGCTCTTACGGGCACTGGCACGGGTGTGTAGTGTGTGTATGTCGGGCG 2942
Db 2880 GTGTCCCGGCTCTTGGGCTTGGCTCGGGTGTGTAGTGTGTGTATGTCGGGCT 2939
QY 2943 GAGAAGGCCACCACTCGACTGTCTCAAGATGTGGCAAGAGGGCTTACCTGTGT 3002
Db 2940 GAGAAGGCCACCACTCGGCTGTCTCAAGATGTGTGCCAGAGGACTTATTTGTTC 2999
QY 3003 GACCAATGGGCTCTTTCGCGCTGTCAAGAGCGCTGTGTGGAATGGACGCGGT 3062
Db 3000 GATCATATGGGCTCTTTCGCGCTGTCTCAAGAGCGCTGTGTGGAATGGACGCGGT 3059
QY 3063 TTTGAGGCTTGTCTTCACTAGGAGGACTGTCCGATCATCAGAGATGCCCGGAGGACC 3122
Db 3060 CTGGAACCTCTCTCATCTACTAGGAGGACTGTCTGATCATACGCGGATCCCGGAGGACT 3119
QY 3123 CTGTCTCGGACAGTGGCTATGGTGTACCCGTGTGTAGCACGCGCGGTGATGAGTT 3182
Db 3120 TTGTCTCGGCGAGTGGCTCATGGTTTACCCGTGTGTGCGCGCTGTGTGATGAGTT 3179
QY 3183 CTCTATCGGCTCTTTCAGGATGTAATCATTTGCTTCCCGGTGTGTCCCGACTGCACCA 3242
Db 3180 CTCTATCGGCTCTTTCAGGATGTAATCATTTGCTTCCCGGTGTGTCCCGACCGCGCT 3239
QY 3243 GTTGTATCCCTCGGTGGGAAAGGCTTCTTGGGGTCAAGAGGAGCTTTCAGAGT 3302
Db 3240 GTTGTATCCCGAGTGGGAAAGGCTTCTTGGGGTCAAAAGGCTGCCCTTTCAGAGT 3299
QY 3303 AGGGATCTGACTTACATCCAGGAAAGCTGTGTGTGGGACGCTACGTACAGAAC 3362
Db 3300 CGGGATCTGACTTACATCCAGGAAAGCTGTGTGTGGGACGCTACGTTCGGAAGC 3359
QY 3363 ATGGGACATGTCTGAATGGCTGTGTTCACAACTTTCCATGGGGTTCATCCCGAAC 3422
Db 3360 ATGGGAACATGTCTGAAGGCTGTGTTCACAGCTTCCATGGGGTTCATCCCGAAC 3419
QY 3423 ATCGGACCGCTGGGGCTTAAATCCAGGTGTGTGTCAGGAGTGTATGATGATGTCAGG 3482
Db 3420 ATCGGACCGCTGGGGCTTAAATCCAGGTGTGTGTCAGGAGTGTATGATGATGTCAGG 3479
QY 3483 GTGTACCGCTTCCAGATGGGCAACTTGTGTGAGCCCTGACCTTGCAGCGGAGTCC 3542
Db 3480 GTGTACCGCTTCCAGATGGGCTTGTGTGTAACACCTTGTACTTGCAGGCTGAGTCC 3539
QY 3543 TGTGGGTATTTAGATCCGAGCGGCTTTTGTGCCATGCTTGTGCAAGGGGACAGGTT 3602

Db	6840	GAGAAATGCTCGGAGGATTCCTGAACCGCACATTGATGTCATCATGAGGACATGCAGTACA	6899
Qy	6903	CCCTCTCTTTGTGGGAGTAGCCGAGAGATGCCCTGTGTGGGGAAGACATATACCCCGCACT	6962
Db	6900	CCCTCTCTTTGTGGTAGTAGCCGAGAGATGCCCTGTATGGGAGAGACATCCCCCGTACT	6959
Qy	6963	CCATPGCCAGCACTTATCTCGGTTACTGAGAGACGCCAGATAGAGAAGACCCCTCGGTG	7022
Db	6960	CCATPGCCAGCACTTATCTCGGTTACTGAGAGACGCTCAGATGAGAAGACCCCGTCGGT	7019
Qy	7023	TCCTCTTCGACAGAGATACCCCGTCTTCTGACTCATTTGCGAGGTCAATCCAGAGTCCGAG	7082
Db	7020	TCCTCTTCGACAGAGATACCCCGTCTTCTGACTCATTTGCGAGGTCAATCCAGAGTCCGAG	7079
Qy	7083	ACGCCGAAGGGAGGAAGCGTCTTCAAGGTGGCTTTTCCGTACTAAAAGCCTCTGTT	7142
Db	7080	ACAGCCGAAGGGAGGAAGTGTCTTCAAGGTGGCTTTTCCGTATTTAAAAGCCTTATTT	7139
Qy	7143	CCACAGAGCATGCCACAAGAAGCTTACCGTTAAGATGTCATGCTGTGTTGAGAAGAGC	7202
Db	7140	CCACAGAGCAGCGACCGACAGGAGCTTACCGTCAAGATGTCGTGCTGCGTTGAAAAGAGC	7199
Qy	7203	GTAACAGCCTCTTTTCATTGGGATTTGACGGTCTGCTGACGTGGCAAGCCTCTGTGAGATG	7262
Db	7200	GTCACGCGCTTTTCTCATTTGGGTTGACGGTGGCTGATGTTGCTAGCGTCTGTGAGATG	7259
Qy	7263	GAATCCAGAACCATACAGCCTATTGTGACAAGGTGCCACTCCGCTTGAAATCCAGGTT	7322
Db	7260	GAATCCAGAACCATACAGCCTATTGTGACAGGTGGCACTCCGCTTGAAATTCAGCGTT	7319
Qy	7323	GGGTGCTTGTGGGCAATGAACCTTACCTTTGAATGTGACAAGTGTGAGGCTTAGGCAAGAG	7382
Db	7320	GGGTGCTTGTGGGCAATGAACCTTACCTTTGAATGTGACAAGTGTGAGGCTTAGGCAAGAA	7379
Qy	7383	ACCTTGGCTTCTTCTCTACATTTGGTCTGGGTGGCACTGACAGAGGGCCACTTCCGGCC	7442
Db	7380	ACCTTGGCTTCTTCTCTACATTTGGTCTGGAGTGGCGCTGACTTAGGCGCCACGCGGCC	7439
Qy	7443	AAGCCCCCTGCTGAGGCGGTGGCTCTTCTGCTGTTGGCGGACACACCAAGGCTGAT	7502
Db	7440	AAGCCTCCGCTGCTGAGGCGGTGGCTCTTGTGTAGTGGCGGACACTTAAAGGTGTAT	7499
Qy	7503	GTCAACCAACCGGACAAATGTGGGAGAAAGTTGACAAGTTTACCTTCTGGCGTGCCTCT	7562
Db	7500	GTTACCAATCCAGCAATGTGGGACGAGGTTGGACAGGTGACCTTCTGGCGTGTCTCT	7559
Qy	7563	AGGTTTCATGACAAATTCCTCTGTGGACTCCATAGAGCGCGTTAAGAGGGCAGCTCAAGCC	7622
Db	7560	AGGTTTCATGATAAGTACCTCTGTGGACTCTATTAGCGCGCTAAGAGGCGCGCTCAAGCC	7619
Qy	7623	TGCTTAAGCATGGTTACACTATAGGAGGCAATAAGGACTGTAAAGGCCACATGCTGCC	7682
Db	7620	TGCTTAAGCATGGTTACACTATAGGAGGCAATAAGGACTGTAAAGGCCACATGCTGCC	7679
Qy	7683	ATGGCTTGGGATCTAAGGTGTGCGTCAAGGACTCGCACCCCTTGCGGGGAAGATGGCT	7742
Db	7680	ATGGCTTGGGATCTAAGGTGTGCGTTAAGGACTTTAGGACTTAGCCACCCCGGGGAAGATGGCC	7739
Qy	7743	GTCCATGACCGGCTCCAGGAGATACTTTGAAGGGACGCCAGTCCCTTTACTCTTACTGTG	7802
Db	7740	GTCCATGACCGGCTTCAGGAGATACTTTGAAGGGACTCCGCTCCCTTTACTCTTACTGTG	7799
Qy	7803	AAAAGGAAGTGTCTTCAAGACGCCAAAGGAGAGAGAGGCCCGCCGCTCATTTGTTTC	7862
Db	7800	AAAAGGAGGTGTCTTCAAGACCGGAAGGAGAGAGGCCCGCCGCTCATTTGTTTC	7859
Qy	7863	CCCCCTTGACTTCCGGATAGCTGAAAAGCTTATTCTGGGAGACCTGTGACGGGTAGCC	7922
Db	7860	CCCCCTTGACTTCCGGATAGCTGAAAAGCTTATCTTTGGGAGACCCAGCGGGGTAGCC	7919
Qy	7923	AAGCGGTGTGTGGGGGGGCGCTACGCTTTCAGTACACCCCAAAATACAGCAATTAGGAG	7982

Db 7920 AAGCGGTGTTGGGGGGCCCTACGCCCTTCAGTACACCCCAAAATCAGCGAGTTAAGGAG 7979
Qy 7983 ATGCTCAAACTGTGGGAATCAAGAAGACACCATCGCCCATCTGTGTGGACGCCACATGC 8042
Db 7980 ATGCTCAAGCTATGGGACTTAAGAAGACCCCTTGCCCATCTGTGTGGACGCCACCTGC 8039
Qy 8043 TTCGACAGTACGATACTGAAGAGGAGCGTGGCGTGTGAGACAGAGCTTTATGCCCCCTGGCT 8102
Db 8040 TTCGACAGTACGATACTGAAGAGGAGCGTGGCGTGTGAGACAGAGCTATACGCTCTCGCC 8099
Qy 8103 TCAGACCATCCAGAAATGGGTGCGCTGGGGAATACTGCTCTGGCACAAATGGTA 8162
Db 8100 TCTGACCATCCAGAAATGGGTGCGGCACTTGGGAAATACTATGCTTCAGGACCATGGTC 8159
Qy 8163 ACCCCGAGGGGGTCCAGTGGGTGAGAGGTATTGTAGATCCTCAGGGGCTTTGACCACC 8222
Db 8160 ACCCCGAGGGGGTCCCGTGGGTGAGAGGTATTGAGATCCTCGGGTGTCTTAACAAT 8219
Qy 8223 AGTCGGAGCAACTGCTTGACTTGCTATATCAAGGTGAAGCCGGCTGTGAGAGGGTGGG 8282
Db 8220 AGCGGAGCAACTGCTTGACTTGCTATCAAGGTGAAGGTGCTGTGAGAGAGTGGG 8279
Qy 8283 CTGAAATGCTCGCTCCATCGCTGGGATGACTGTTGATCATATGGAACGGCT 8342
Db 8280 CTGAAATGCTCGCTCCATCGCGGGATGACTGCTTGATCATATGAGCGGCCA 8339
Qy 8343 GTGTCCGATCTAGCGACGCTTTGGGAGAGCCCTGGCGAGCTACGGGTACGATCGGAG 8402
Db 8340 GTGTCCGACCAAGGACGCTTTGGGAGAGCCCTAGCGAGCTATGGGTACGCGTGGAG 8399
Qy 8403 CTTTCGATCATGATCACTGAGACACGGCCCTTCTGCTCCACTTGGCTAGCTGAGTGC 8462
Db 8400 CCTTCATATCATGATCATTTGGACACGGCCCTTCTGCTCCACTTGGCTAGTGC 8459
Qy 8463 AATCAGATGGAAAGCCCATTTCTTCTGACACGACGACTTCGGAGGCCCTCGCTCGC 8522
Db 8460 AATCAGATGGAAAGCCCATTTCTTCTGACACGACGACTTCGGAGGCCCTCGCTCGC 8519
Qy 8523 ATGTGACGAGTACAGTACCAATGGCTTCGGCCATCGGTTACATCTCTTATACCT 8582
Db 8520 ATGTGAGTATAGTACCCGATGGCTTCGGCGATCGGTACATCTCTTATCT 8579
Qy 8583 TGGCATCTATCACCGGTGGGTGATCATCCCTCACGTGCTACCTTCGCGCTTTAGGGGT 8642
Db 8580 TGGCACCCCATCACAGTGGGTGATCATCTCTCATGTGCTAACGTGCGCATTCAGGGT 8639
Qy 8643 GGTGGCACCGCTGATCTGCTGTGTGGTCCAGGTATGTTACTACAAGTTTCCA 8702
Db 8640 GGAGGCACCGCTGATCGGGTTGTGGCCAGGTGATGTTACTACAAGTTTCCA 8699
Qy 8703 CTGGACAACTGCTAACTCATCTGCTGCGCTCCACGGACGACGAGGTTGAGGGTTACC 8762
Db 8700 CTGGACAACTGCTAACTCATCTGCTGCGCTCCACGGACGACGAGGTTGAGGGTTACC 8759
Qy 8763 GCAGACAACTAAGACAAAATGAGGCTGGCAAGTGTGAGCGACCTCAAGCTCCCT 8822
Db 8760 GCAGACAACTAAGACAAAATGAGGCTGGTAAAGTCTTGAGCGACCTCAAGCTCCCT 8819
Qy 8823 GGCCTAGCAGTCCACCGAAGAGCCGGGCGATTTGCGAGCGGTATGCTCCGGTCCGGC 8882
Db 8820 GGCCTAGCAGTCCACCGAAGAGCCGGGCGTTCGGAACACGCAATGCTCCGGTCCGGC 8879
Qy 8883 GGTGGGCTGAGTTGGTATAGGGGCTGTGTGGGCTCCAGCGCTTCGCGCTTCCCGCTCCG 8942
Db 8880 GGTGGGCTGAGTTGGTATAGGGGCTGTGTGGGCTCCAGCGCTTCCCGCTTCCCGCT 8939
Qy 8943 GAGATTGCTGATPCCCCGGGGTTTCCCCCTTTCGCCCCCTATATATGGGGTGGTTTAT 9002
Db 8940 GAGATTGCTGATPCCCCGGGGTTTCCCCCTTTCGCCCCCTATATATGGGGTGGTTTAT 8999
Qy 9003 CAATTGATTTCAACGCCAGAGAGTGCCTGGCGGTGGTTGGGTTCTTAGCCCTGCTC 9062
Db 9000 CAATTGATTTCAACGCCAGAGAGTGCCTGGCGGTGGTTGGGTTCTTAGCCCTGCTC 9059

Qy 9063 ATGCTAGCCCTTTCGGGTGAACCTAAATTCATCTGTTGCGCAAGGTTCGGTGAATGATC 9122
Db 9060 ATGCTAGCCCTTTCGGGTGAACCTAAATTCATCTGTTGCGCAAGGTTCGGTGAATGATC 9119
Qy 9123 ATCAGTGGAGAGGTTCCCGCCCTCCCGCCCGCCAGGGGTCTCCCGCTGGGTAAAAGG 9182
Db 9120 ATCAGGAGAGGTTCCCGCCCTCCCGCCCGCCAGGGGTCTCCCGCTGGGTAAAAGG 9179
Qy 9183 CCCGGCTTCGGAGGATGTTGTTACTAACCCCTGCGAGGTTCAAGGCTGATGTTGC 9242
Db 9180 CCCGGCTTCGGAGGATGTTGTTACTAACCCCTGCGAGGTTCAAGGCTGATGTTGC 9239
Qy 9243 TAATGCACTGCCACTTCGGTGGCGGTCGCTACCTTATAGCTTAATCCGTGACTACGGC 9302
Db 9240 TAATGCACTGCCACTTCGGTGGCGGTCGCTACCTTATAGCTTAATCCGTGACTACGGC 9299
Qy 9303 TGCTCGAGAGCCCTCCCGGATGGGCGACAGTGCAGTGTGATCTGAAGGGGTGCACCC 9362
Db 9300 TGCTCGAGAGCCCTCCCGGATGGGCGACAGTGCAGTGTGATCTGAAGGGGTGCACCC 9359
Qy 9363 GGTAAAGAGCTCGGCCAAAGCGCGGTTCTACT 9395
Db 9360 GGTAAAGAGCTCGGCCAAAGCGCGGTTCTACT 9392

RESULT 5

AA02334
ID AAX02334 standard; cDNA; 9392 BP.
XX
AC AAX02334;
XX
DT 06-MAY-1999 (first entry)
XX
DE US5856134 Seq ID 14.
XX
KW Non-A Non-B Non-C Non-D Non-E Hepatitis Virus; immunogen; HGV; HAV; HBV;
KW immunoreactive; serum alanine aminotransferase; hepatitis A virus; HCV;
KW hepatitis B virus; hepatitis C virus; hepatitis D virus; HDV; HEV;
KW hepatitis E virus; Flaviviridae; prophylactic; therapeutic; diagnosis;
KW antibody; vaccine; detection; ds.
XX
OS Hepatitis G virus.
XX
FH Key Location/Qualifiers
FT CDS 459..9080
FT /tag= a
FT /product= "HGV-PNF 2161 variant"
XX
PN US5856134-A.
XX
PD 05-JAN-1999.
XX
PF 05-JUN-1995; 95US-0461361.
XX
PR 19-MAY-1995; 95US-0444733.
PR 20-MAY-1994; 94US-0246985.
PR 03-AUG-1994; 94US-0285543.
PR 03-AUG-1994; 94US-0285558.
PR 03-AUG-1994; 94US-0285561.
PR 26-OCT-1994; 94US-0329729.
PR 23-NOV-1994; 94US-0344271.
PR 16-DEC-1994; 94US-0357509.
PR 15-FEB-1995; 95US-0389886.
PR 05-JUN-1995; 95US-0461361.
XX

(GENE-) GENELABS TECHNOLOGIES INC.

Fry KE, Kim JP, Linnen JM, Wages J, Young LM;

WPI; 1999-105108/09.

P-PSDB; AAW92755.

XX

PT New isolated hepatitis G virus antigens - used to develop products
PT for the diagnosis, prophylaxis and therapy of hepatitis G virus
PT infections
XX

PS Example 6; Column 99-118; 204pp; English.

XX This invention describes a Non-A Non-B Non-C Non-D Non-E Hepatitis Virus
CC (HGV) immunogenic composition which comprises a purified HGV polypeptide
CC antigen at least 10 amino acids in length which is specifically
CC immunoreactive with HGV-positive sera, present in a carrier, where HGV
CC is characterised by (a) production of elevated serum alanine
CC aminotransferase levels in an infected primate (b) its serological
CC distinction from hepatitis A virus (HAV), hepatitis B virus (HBV),
CC hepatitis C virus (HCV), hepatitis D virus (HDV), and hepatitis E virus
CC (HEV) (c) membership in the virus family Flaviviridae. The compositions
CC can be used to develop products useful for prophylactic, therapeutic and
CC diagnosis applications. The immunogenic compositions can be used for the
CC production of antibodies. In vaccines and for detection and diagnosis.
XX

SQ Sequence 9392 BP; 1694 A; 2551 C; 2998 G; 2148 T; 1 other;

Query Match 84.9%; Score 7979; DB 20; Length 9392;

Best Local Similarity 90.7%; Pred. No. 0;

Matches 8515; Conservative 1; Mismatches 876; Indels 1; Gaps 1;

QY 3 ACCTGGGGGGTGTATCCCGCCCGGACCTGGGTGCAAGGCCCATAAACCGAGCCCT 62
DB 1 ACCTGGGGGAGTGTATCCCGCCCGGACCTGGGTGCAAGGCCCATAAACCGAGCCCT 60
QY 63 ATCTAAGTAGACCAATGACTCGGGCCGACCTCGGCGACCGCGCAAAAGGTGGTAGTG 122
DB 61 ATCTAAGTAGACCAATGACTCGGGCCGACCTCGGCGACCGCGCAAAAGGTGGTAGTG 120
QY 123 GTGGTCACAGGTTGCTAGTCTTAATCCCGTCACTCTGCTAGCCACTATAGTGGGT 182
DB 121 GTGATGACAGGTTGCTAGTCTTAATCCCGTCACTCTGCTAGCCACTATAGTGGGT 180
QY 183 CTTAAGAGAAGGTCAAGACTCTCTTGTGCTCGGCGAGACCGCGACGGTCCACAGGT 242
DB 181 CTTAAGAGAAGGTCAAGACTCTCTTGTGCTCGGCGAGACCGCGACGGTCCACAGGT 240
QY 243 GCTGGCCCTACCGGTGTGAATAGGCGCGACGTAGGCTGCTGTAAACCGAGCCCGT 302
DB 241 GTTGGCCCTACCGGTGGGAATAAGGCGCGACGTAGGCTGCTGTAAACCGAGCCCGT 300
QY 303 CACCCACCTGGGCAACGAGCGCCAGTACGCTCAGGTCACGTCGCCCTTCAATGCTCTCTTG 362
DB 301 TACCCACCTGGGCAACGAGCGCCAGTACGCTCAGGTCACGTCGCCCTTCAATGCTCTCTTG 360
QY 363 ACCAATAGGTTTATCGGCGAGTTGACAAGGACCAAGTGGGGCGCGGGGTATGGGAAG 422
DB 361 ACCAATAGGCGTAGCGGCGAGTTGACAAGGACCAAGTGGGGCGCGGGGT-TGGAGAGG 419
QY 423 GACCCCAACCCCTGCCCTTCCCGGTGGGGGGAATGATGGGGCGACCCAGCTCCGG 482
DB 420 GACTTCAAGTCCCGCTTCCCGGTGGGGGGAATGATGGGGCGACCCAGCTCCGG 479
QY 483 CGCGCTCGAGCGGGGTAGCCCAAGATCTTCGGGTGAGGGCGGGTGGCACTTCTCTT 542
DB 480 CGCGCTCGAGCGGGGTAGCCCAAGATCTTCGGGTGAGGGCGGGTGGCACTTCTCTT 539
QY 543 TTCTATACCATCATGCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 602
DB 540 TTCTATACCATCATGCGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 599
QY 603 GCGCGCGCCACCGTGTGCGAGCAATGGGCAATATTTCTCAAAATTCCTGTGCC 662
DB 600 GCGCGCGCCACCGTGTGCGAGGCAATGGGCAATATTTCTCAAAATTCCTGTGCC 659
QY 663 CCGGAAGACATCGGTTCTCGCTGGAAGCGGATGCTGTGGCCCTGGGGTCACGGTT 722
DB 660 CCGGAGACATCGGTTCTCGCTGGAAGCGGATGCTGTGGCCCTGGGGTCACGGATT 719

QY 723 TGCACCGACCGTTGGTGGCCACTGTATCAGCGGGTGTGGCTGTGGCGCTGCAAGTCC 782
DB 720 TGCACCTGACCAATGCTGGCCACTGTATCAGCGGGTGTGGCTGTGGCGCTGCAAGTCC 779
QY 783 GCGGCCACGCTGTTGGGGAACCTGTAGCGGCCCTTGTGGGTCTCGGCTTAC 842
DB 780 GCGGCCCAACTGCTGGGAGCTGGGTAGCTATACGGGCCCTGTGCGTCTCGGCTAT 839
QY 843 GTAGCCGGATCTCGGCTGGGAGGTTACTCGGGGTCTGACAGTGGTGGTGG 902
DB 840 GTGGCTGGATCTCGGCTGGGAGGTTACTCGGGGTCTGTAACGGTGGAGTGG 899
QY 903 TTGAGCGCGCGGTCTACCTGATGCCCAACTCAAGTGTGACGTAGATGTGACGTAA 962
DB 900 TTGACGCGCGGTCTACCGGTGCTTAACCTGACGTGTCAGTGGGTGAGCTAAAG 959
QY 963 TGGGGAAGTGTGTTGGAGATGAGTGTGAGTGTGGCTTCCCAATTTACTGATTTGGAA 1022
DB 960 TGGGAAAGTGTGTTGGAGATGAGTGTGAGTGTGGCTTCCCAACTTACTGATTTGGAA 1019
QY 1023 TACCTTTGNAAGTCCCATTTGATTTTGAGAGGAGTGTGACCTGACCCCTCTGTTG 1082
DB 1020 TACCTTGAAGTCCCATTTGATTTTGAGAGGAGTGTGATAAGCCTGACCCCTTGTG 1079
QY 1083 GTTGGGTGGCCCATTTGCTTTGCTGGAGCAACGGATGTCATGTTTCTCTGCTGGTG 1142
DB 1080 GTTGGGTGGCCCATTTGCTTTGCTGGAGCAACGGATGTCATGTTTCTCTGCTGGTG 1139
QY 1143 ACGATGGCGGGATGTTGCAAGCGCCCGCTCGCTTTTGGGGTCCCGCCCTTTGAC 1202
DB 1140 ACGATGGCGGGATGTTGCAAGCGCCCGCTCGCTTTTGGGGTCCCGCCCTTTGAC 1199
QY 1203 TAGCGGTGAGTGGGAGTCTCTCTGAGGGCTAAACGGTTCGCTATTTCCACTGGG 1262
DB 1200 TAGCGGTGAGTGGGAGTCTCTCTGAGGGCTAAACGGTTCGCTATTTCCACTGGG 1259
QY 1263 GAGAGGTGTGGATCGAGGGAATGTGACGCTCTTGTGACTGCCCAACGGCCCTGG 1322
DB 1260 GAGAAGTGTGGGACCTGGGAACGTTACGCTTTCAGTGTGACTGCCCTAACGGCCCTGG 1319
QY 1323 GTTGGGTCCCGCCCTTTTGGCAGGCGGTGGGTGGGGCGACCCCATCACCATTGGAGC 1382
DB 1320 GTGTGTTGCCACCTTTTGGCAAGCAATCGGCTGGGGTGAACCCCATCACTTATTGAGC 1379
QY 1383 CACGCAAAACACGATGGCCCTTATCATGCCCAATATGCTATGGGTCTGTGCTCGTA 1442
DB 1380 CACGCAAAACACGATGGCCCTTATCATGCCCAAGTATGCTATGGGTCTGTACAGTC 1439
QY 1443 ACGTGTGTGGGTTCGCTGCTTGTGCTTGTGCTGACCGGGCTGTGATTCGAAGATC 1502
DB 1440 ACTTGTGTGGGTTCGCTGCTTGTGCTTGTGCTGACCGGGTTCGCGACTCGAAGATA 1499
QY 1503 GATGTGTGAGTGTGGTGGCGGTGGATCTCCGAGTGGGAGTCCCGTCCGTAACGTGTATT 1562
DB 1500 GATGTGTGAGTGTGGTGGCGGTGGATCTCCGAGTGGGAGTTCGCGACTCGAAGATA 1559
QY 1563 TCGGATCGGACACGCTGTGAGTCTCCGAGTGGGAGTCCCGTCCGTAACGTGTATT 1622
DB 1560 TCGGATCGGACACGCTGTGAGTCTCCGAGTGGGAGTTCGCGACTCGAAGATA 1619
QY 1623 CTGACCGTGGCCCTGCTTCAATGTGCACTGTGTGCGGGAGTGTGCGCCGCAACCGGG 1682
DB 1620 CTGACCGTGGCCCTGCTTCAATGTGCACTGTGTGCGGGAGTGTGCGCCGCAACCGGG 1679
QY 1683 TCGGTTAGATTCCTTCCATCGGTGGGACCGGGCTCGGCTGACAAAGGACTTGGAA 1742
DB 1680 TCGGTTAGATTCCTTCCATCGGTGGGAGTTCGCGCTGACAAAGGACTTGGAA 1739
QY 1743 GCTGTGCCCTTCTCAACAGGACAATCTCCATTAAGGCGCCCTTGGGCAACCGAG 1802
DB 1740 GCTGTGCCCTTCTCAACAGGACAATCTCCATTAAGGCGCCCTTGGGCAACCGAG 1799
QY 1803 GGGAGAGGCAACCGGTTGGGTGCGCCCTGGGTCTTGGGTCTTACACCATGACCAAGATC 1862

QY 4023 TCGCCCTTACCTATTCCACTTACGAAAGGTTTTTGGCCAAACCCCTAGGCAGATGCTGAGG 4082
DB 4020 TCCCCCTTACCTATTCCAACTTATGGGAGGTTTTTGGCCAAACCCCTAGGCAGATGCTAGCG 4079
QY 4083 GGTGTGTCGGTGTCTATTGTGACGAGTGCCACAGTCATGACTCAACTGTGTGTTGGGC 4142
DB 4080 GSCGTTTCGGTGTCTATTGTGATGAGTGCCACAGATCATGACTCAACGCTGCTGTAGGC 4139
QY 4143 ATTGGGCTGTACGAGGCTGCGCGGAGGATGTGAGTGCAATTTGGTGTCTACGCCACT 4202
DB 4140 ATTGGGAGAGTCCGGAGCTGCGCGGTGGGTGCGGGGTGCAACTAGTGTCTTACGCCACC 4199
QY 4203 GCCACCTCCCGGATCCCGGATGACCAGACCCATCAATCATTTAGACAAACTGGAC 4262
DB 4200 GCTACACCTCCCGGATCCCTTATGACGACGACCCCTTCATTAATTGAGACAAATTTGGAC 4259
QY 4263 GTGGGAGAGATCCCTTCTATGGGCATGGCATPACCTCTTTGAGCGGATGCGGACCGGAAGG 4322
DB 4260 GTGGGCGAGATTCCCTTTTATGGGCATGGAATACCCCTCGAGCGGATGCGGAACCGGAAGG 4319
QY 4323 CATCTCGTATTCTGCCACTCCAAAGCTGAGTGGAGCGCCTGGCGGGCCAGTTTTCGGCT 4382
DB 4320 CACCTCGTGTCTGCGCATTTCTAAGGCTGAGTGGAGCGCCTTGTCTGGCCAGTTCTCCGCT 4379
QY 4383 AGGGGGTAAATGCCATCGCCTATTACAGGGGAAAGACAGTTCTATCATCAAAGATGA 4442
DB 4380 AGGGGGGTCAATGCCATTGTCCTATTATAGGGGTAAAGACAGTTCTATCAATCAAGATGG 4439
QY 4443 GACCTGGTGTGTGCTACAGACACTATCCACTGGGTACACTGGGAACCTTCGATTCT 4502
DB 4440 GACCTGGTGTGTGCTACAGACGCGCTTTCACCTGGGTACACTGGAAATTTTCGACTCC 4499
QY 4503 GTACCGGATTGGGCTTAGTGTGGAGGAGTCTCGAGGTACACCTTGATCCCAACATT 4562
DB 4500 GTACCGGACTGTGGGATTAGTGTGGAGGAGTCTGTGAGGTGACCTTGATCCCAACATT 4559
QY 4563 ACCATCTCCCTCGCACGCTGCCGCTCGGCTGAACCTGTGATGACGCGCGAGGAGCG 4622
DB 4560 ACCATCTCCCTCGCACAGTGCCTCGCTCGGCTGAACCTGTGATGCAAGACGAGGACGC 4619
QY 4623 ACGGCTAGGGCAGTCTGGGCGCTACTACTACGCGGGGGTCGGAAGCCCTCTGCTGT 4682
DB 4620 ACGGCTAGGGCAGTCTGGGCGCTACTACTACGCGGGGGTCGGAAGCCCTCTGCGGT 4679
QY 4683 GTGGTGCCTCAGTCTGTCTGTCTGCTGCGGCTGGAAGCGGTGACCTGGTACGGAATG 4742
DB 4680 GTGGTGCCTCAGTCTGTCTGTCTGCTGCGGCTGGAAGCTGGAGTGACCTGGTACGGAATG 4739
QY 4743 GAACTGACCTGACAGCAACCTACTGAGACTTTTACGACAACCTGCGCTTACACCGCAGCC 4802
DB 4740 GAACTGACTTGACAGCTAACTACTGAGACTTTTACGAGACTGCGCTTACACCGCAGCC 4799
QY 4803 GTCCAGCTGACATTTGGGGAAGCCGCGGTGTTCTTTTTCGGGCTTTCGCCCTTGAGGATG 4862
DB 4800 GTCCGCGGTGATATGGGAAGCCGCGGTGTTCTTCTCTGGGCTCGCCCAATTGAGGATG 4859
QY 4863 CATCCGATGTAGCTGGGCAAAAGTTCCGCGCGTCACTGCGCCTTCTGTGTGGGTGT 4922
DB 4860 CACCTGATGTAGCTGGGCAAAAGTTCCGCGCGTCACTGCGCCTTCTGTGTGGGTGT 4919
QY 4923 CAGCGGACCATGTGCGGGGAAACACTGTCTCCCGGCCATCGATGACCCCAAGTGGCA 4982
DB 4920 CAGCGGACCATGTGTGCGGGAACACTGTCTCCCGGCCATCGATGACCCCAATGGCA 4979
QY 4983 GGTCTGAAGGGCCGAATCTCTCCACTCTCTGCTGAGGTGGGCAATGATTTACCATCT 5042
DB 4980 GGTCTGAAGGGCCGAATCTCTCTCCACTCTCTGCTGAGGTGGGCAATGATTTACCATCT 5039
QY 5043 AAAGTGGCGGGCCATCATCTGTGACGACCTGTGTCGCTAGGCTCGGGGTGCGGAGGT 5102
DB 5040 AAAGTGGCGGGCCACATAGTGGACGACCTGGTCCGAGACTCGGTGTGCGGAGGT 5099

QY 5103 TACGTCGCTGCGATCGCGGACCCCATCTTGATGGTGGGCTCGCTATTTCGGGGGCGCATG 5162
DB 5100 TACGTCGCTGCGAGCTGGCGCGATCTTGATGATCGGTCTAGCTATATCGGGGGGAATG 5159
QY 5163 ATCTATGCGCTATACACCGGGTCTCTCTGCTGGTGGTTACAGACTGGGATGTGAAGGGGGT 5222
DB 5160 ATCTACGCGTATACACCGGGTCTAGTGGTGGTGACAGACTGGGATGTGAAGGGGGT 5219
QY 5223 GGCAGCGCCTTTATTCGGCATGGAGACAGGCGACGCCCGCCAGCGGTTGTGAGGTCCCC 5282
DB 5220 GGCAGCGCCTTTATTCGGCATGGAGACAGGCGACGCCCTCAGCGGTTGTGAGGTCTCT 5279
QY 5283 CCGGTAGACCATCGCGCGGGGAGAGTCTGCGCATCGGATGCGCAACACAGTGCAGAT 5342
DB 5280 CCGGTAGACCATCGCGCGGGGGTGAATCAGCACCATCGGATCGCAAGACAGTGCAGAT 5339
QY 5343 GCGGTGGCGGCOATCAGGTGGATTCCGATTGGTTCAGTTCAGTTCAGTTCGATCGGGGAA 5402
DB 5340 GCGGTGGCAGCCATCCAGGTGGACTGCGATTGGACTATCATGACTCTGTCTCGATCGGAA 5399
QY 5403 GTGCTGTCTTGGCCAGGCTAAGACGGCGGAGGCTACGCACTACACCAAGTGGCTT 5462
DB 5400 GTGTTGTCTTGGCTAGGCTAAGACGGCGGAGGCTACACAGCAACCCCGAAGTGGCTC 5459
QY 5463 GCTGCTGTCTACACGGGACGCGCGCTGCCACTGTTTCAATTGTTGACAAGTCTTTC 5522
DB 5460 GCTGCTGTCTACCGGGACGCGCGCTTCCACTGTATCCATGTTGACAAGTCTTTC 5519
QY 5523 GCCGGGCGTGGCGCGGCTGTAGGCCATGCCACAGTGTAAATAGTTCGCGAGTGGCG 5582
DB 5520 GCCGGAGGTGGCGGCTGTGTGGGCCATTTGCCACAGCTGATTGCTCGCGGCTGGCG 5579
QY 5583 GCTATGGGCTTCTAGGAGCCCTCCATTGGCTGCTGCGCTTCTACCTCATGSGGTTG 5642
DB 5580 GCTACGGGCTTCAAGGAGCCCGGCTTGGCAGCGCGGCTTCTTACCTCATGSGGTTG 5639
QY 5643 GCGCTGGAGGACGCGCAACCGCTTAGCTTTCGCTCTCTACTAGGGCGCGCTGGG 5702
DB 5640 GCGCTGGAGGACGCTCAGACGCGCTTCTGCGCTCTCTTATTTGGGGCTGCTGGA 5699
QY 5703 ACGGCTTGGGACGCGCTGCTGGGTTAACATGGCGGGCGGTTCTATGGAAGTGT 5762
DB 5700 ACGGCTTGGGACGCTGCTGCTGGGCTTGGACATGGCAGTCCGTTCTATGSGGGGCGC 5759
QY 5763 ACGGCTTCCCTCTTGGTCACTTTTACTTGGGGCGGCTGGGGCGTGGAGGCGGCTG 5822
DB 5760 AGTGTCTCCCTCTTGGTCACTTTTATTTGGGGCGGCTCGGAGGTTGGGAGGTTGT 5819
QY 5823 GTGAATGGGCTTAGCTTCTTCGACTTTTATGGGGGGAACCTATCATCAGAAGATCTG 5882
DB 5820 GTCAAGCGCGGAGCTAGTCTTTGACTTTCATGCGGGGGAACCTTTCATCAGAAGATCTG 5879
QY 5883 TGGTATGCCATCCCATGCTAACAGTTCGCGGGGAGGACTTTCGCGGGATTCGCCCTCGG 5942
DB 5880 TGGTATGCCATCCCGTACTGACAGCCCGGGGGGCGCTTTCGCGGGATTCGCTCGGG 5939
QY 5943 TTGGTGTCTTACTCAGCTAACAACTTCTGCACTTACCACTTGGTGAACGCTTCTGCTGACT 6002
DB 5940 TTGGTGTCTTACTCAGCTAACAACTTCTGCACTTACCACTTGGTGAACGCTTCTGCTGACT 5999
QY 6003 ACATTGCCAAGCTCTCATGCTTCTTCGACTTTTATGGGGGGAACCTATCATCAGAAGATCTG 6062
DB 6000 AGTTTACCAGGCTTCTATGATCCGAGACAGTACTTTCAGCAAGTTCAGTATTCGAGAC 6059
QY 6063 AAGGTCTCAGCTGTCTCCGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 6122
DB 6060 AAGGTCTCAGCTGTCTCCGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 6119
QY 6123 AGGAGCCTAAGTGGATGAGTTTGGGTTGAGTGTGGGCTTGGGAGTGGGATC 6182
DB 6120 AGGAGCCTAAGTGGATGAGTTTGGGTTGAGTGTGGGCTTGGGAGTGGGATC 6179
QY 6183 ATGCGCTAAGTGGGATGATGGCAGACTTTCGGGGCTTCTGCCCGCTGCTGTCATTA 6242

Qy	8403	CCTTCGTATCATG	CATCACTG	ACAGCGCC	CCCTTCTG	CTCCACTT	GGCTAG	CTAGCTG	C	8462	
Db	8400	CCCTCATATCATG	CATCATTTG	ACAGCGCC	CCCTTCTG	CTCCACTT	GGCTAG	CTAGCTG	C	8459	
Qy	8463	AATGCAGATGG	AAAGCCGATTTCTT	CTGTGAC	ACCGAGCTTTCG	AGGAGCC	CTCGCTCG			8522	
Db	8460	AATGCAGATGG	AAAGCGCATTTCTT	CTGTGAC	ACCGAGCTTTCG	AGGAGCC	CTCGCTCG			8519	
Qy	8523	ATGTGAGCGAG	TACAGTGAC	CAATGGTTCG	GCGCATCGG	TATCATCTC	CTTATAC	CC		8582	
Db	8520	ATGTGAGTGAG	TATAGTAC	CAACGATGGTTCG	GCGCATCGG	TATCATCTC	CTTATAC	CC		8579	
Qy	8583	TGGCATCCCT	ATCACACG	TGGGTGCATC	ATCCCTAC	GTGCTCAC	CTGGCGCTTT	AGGGT		8642	
Db	8580	TGGCACCCAT	CACACG	TGGGTGCATC	ATCCCTCAT	GTGCTAAC	GTGGCATTC	AGGGT		8639	
Qy	8643	GTGTGGCAC	ACGFTGATC	CTCTGTGTG	TGCCAGGTAC	ATGTAAT	ACTACA	AGTTTCCA		8702	
Db	8640	GGAGGCAC	ACCGTCTG	ATCCGGTTTGG	TGCCAGGTGC	ATGTAAT	ACTACA	AGTTTCCA		8699	
Qy	8703	CTGGACAACT	GTGCTAA	CATCATCTG	TGGCCCTCC	ACGACG	CAGCAG	CGTTT	AGGTTACC	8762	
Db	8700	CTGGACAACT	GTGCTAAC	CATCATCTG	TGGCCCTCC	ACGACG	CAGCAG	CGTTT	AGGTTACC	8759	
Qy	8763	GCAGACAACT	TAAGAC	AAAAATG	GAGGCTG	GCAAGGTG	CTGACG	AGACTCA	AGCTCCCT	8822	
Db	8760	GCAGACAACT	TAAGAC	AAAAATG	GAGGCTG	GTAAGTTCT	GAGGAC	CTCAAG	CTCCCT	8819	
Qy	8823	GGCCTAGC	AGTCCAC	CGGAAG	AGCGCGG	GATTTG	CGAACG	CGTATG	CTCCG	CTCGGC	8882
Db	8820	GGCTTAGC	AGTCCAC	CGAAG	AGCGCGG	GATTTG	CGAAC	CGCATG	CTCCG	CTCGGC	8879
Qy	8883	GGTTGGCT	GAGTTGG	CTAGG	GGGCTGTTG	TGGCTCC	CAGAG	CTCGG	CTTCC	CCCTCCG	8942
Db	8880	GGTTGGCT	GAGTTGG	CTAGG	GGGCTGTTG	TGGCATC	CAGAG	CTCGG	CTTCC	CCCTCC	8939
Qy	8943	GAGATTGCT	TGTTAT	CCCCGGG	GGTTTCC	CCCTTTCC	CCCCCTAT	ATATG	GGGGTGG	TTTCAT	9002
Db	8940	GAGATTGCT	TGTTAT	CCCCGGG	GGTTTCC	CTCTCTCT	CCCCCTAT	ATATG	GGGGTGG	TTTCAT	8999
Qy	9003	CAATTGGATT	TCACAAG	CCACAG	AGGAGT	CTGCTGG	CGGTGGT	TGAG	CGCTG	CTGTC	9062
Db	9000	CAATTGGATT	TCACAAG	CCACAG	AGGAGT	CTGCTGG	CGGTGGT	TGAG	CGCTG	CTGTC	9059
Qy	9063	ATCCTAG	CCCTCTT	CGGGTGA	ACTAAAT	TCATCTG	TTCG	GCAAG	GTCCG	GTGACTG	9122
Db	9060	ATCCTAG	CCCTCTT	CGGGTGA	ACTAAAT	TCATCTG	TTCG	GCAAG	GTTCG	GTGACTG	9119
Qy	9123	ATCATTG	GAGAGG	TTCCG	CCCTCC	CCGCCCC	AGGGTCTC	CCCG	CTGGT	GTAAAG	918

XX	AAV82093;	
XX	29-MAR-1999 (first entry)	
XX	Hepatitis G virus PNF 2161 variant CDNA.	
XX	HGV; hepatitis; diagnosis; therapy; vaccine; ds.	
XX	Hepatitis G virus variant PNF 2161.	
XX	Key Location/Qualifiers	
XX	CDS 459..9080	
XX	/*tag= a	
XX	US5849532-A.	
XX	15-DEC-1998.	
XX	06-JUN-1995; 95US-0464134.	
XX	19-MAY-1995; 95US-0444733.	
XX	20-MAY-1994; 94US-0246985.	
XX	03-AUG-1994; 94US-0285543.	
XX	03-AUG-1994; 94US-0285558.	
XX	03-AUG-1994; 94US-0285561.	
XX	26-OCT-1994; 94US-0329729.	
XX	23-NOV-1994; 94US-0344271.	
XX	16-DEC-1994; 94US-0357509.	
XX	15-FEB-1995; 95US-0389886.	
XX	06-JUN-1995; 95US-0464134.	
XX	(GENE-) GENELABS TECHNOLOGIES INC.	
XX	Fry KE, Kim JP, Linnen JM, Wages J, Young LM;	
XX	WPI; 1999-069731/06.	
XX	P-PSDB; AAW89452.	
XX	Vector containing hepatitis G virus nucleic acid - and transformed	
XX	cells for producing recombinant HGV polypeptide	
XX	Claim 1; Column 99-118; 204pp; English.	
XX	This is a consensus sequence of variant PNF 2161 of a newly	
XX	discovered non-A/non-B/non-C/non-D/non-E hepatitis-associated	
XX	viral agent, designated hepatitis G virus (HGV). The sequence was	
XX	deduced from partial clone 470-20-1 (see AAV82094), which was	
XX	obtained by immunoscreening a recombinant library constructed from	
XX	patient PNF2161 serum cDNA, and from overlapping extension clones	
XX	(see AAV82113-32). A vector containing an HGV nucleic acid composed	
XX	of this 9392 bp sequence linked to a control sequence and encoding a	
XX	product at least 10 amino acids in length is claimed. Also claimed	
XX	are a cell transformed with the vector (especially E. coli where the	
XX	vector is phage lambda, or a Spodoptera frugiperda cell where the	
XX	vector is a baculovirus transfer vector), and a method of producing	
XX	HGV polypeptides (see AAW89452) by culturing such cells. HGV is	
XX	characterised by: (i) producing elevated serum alanine	
XX	aminotransferase levels in infected primates; (ii) its serological	
XX	distinction from hepatitis A, B, C, D and E viruses; (iii)	
XX	membership of the family Flaviviridae; and (iv) a viral genome	
XX	having a region that is selectively hybridisable with the 470-20-1	
XX	clone sequence. The recombinant HGV polypeptides can be used as	
XX	antigens for diagnosis of HGV infections, in vaccines and for	
XX	antibody production. Methods are presented for the nucleic acid-	
XX	based detection of HGV in samples and for the isolation of further	
XX	HGV genomic sequences.	
XX	Sequence 9392 BP; 1694 A; 2551 C; 2998 G; 2148 T; 1 other;	
XX	Query Match 84.9%; Score 7979; DB 20; Length 9392;	
XX	Best Local Similarity 90.7%; Pred. No. 0;	
XX	Matches 8515; Conservative 1; Mismatches 876; Indels 1; Gaps 1;	

QY 3 ACGTGGGGGGTGTATCCCGCCCCCGGCACTGGGTGCAAGCCCAATAAACCGACGCT 62
DB 1 ACGTGGGGAGTGTATCCCGCCCCCGGCACTGGGTGCAAGCCCAATAAACCGACGCT 60
QY 63 ATCTAAGTAGACGAATAGCTCGGCGCCGACACTCGCGACCGGCCAAAAGGTGGTATGG 122
DB 61 ATCTAAGTAGACGAATAGCTCGGCGCCGACACTCGCGACCGGCCAAAAGGTGGTATGG 120
QY 123 GTGGTGACAGGTTGGTAGTGGTAAATCCCGGTATCTCTGGTAGCCACTATAGTGGGT 182
DB 121 GTGATGACAGGTTGGTAGTGGTAAATCCCGGTACCTTGGTAGCCACTATAGTGGGT 180
QY 183 CTTAAGAGAAGTCAAGACTCTCTGTGTGCTCGCGGAGACCGCGCACGGTCCACAGGT 242
DB 181 CTTAAGAGAAGTCAAGACTCTCTGTGTGCTCGCGGAGACCGCGCACGGTCCACAGGT 240
QY 243 GCTGGCCCTACCGGTGTGAATGAAGGCGCGACGTCAGGCTGTCTGTTAAACGAGCCCGT 302
DB 241 GTTGGCCCTACCGGTGGGAATGAAGGCGCGACGTCAGGCTGTCTGTTAAACGAGCCCGT 300
QY 303 CACCACCTGGGCAACGACGCCACGTCAGGTCCACGTCGCGCTTCAATGTCTCTCTTG 362
DB 301 TACCACCTGGGCAACGACGCCACGTCAGGTCCACGTCGCGCTTCAATGTCTCTCTTG 360
QY 363 ACCAATAGGTTTATCCGGCGAGTTGACAAGGACCAAGTGGGGCCCGGGTATGGGGAAG 422
DB 361 ACCAATAGGCGTAGCGGCGAGTTGACAAGGACCAAGTGGGGCCCGGGGCT-TGGAGAGG 419
QY 423 GACCCCAACCCCTGCCCTTCCCGGTGGCGGGAATGATGGGGCCACCGACGTCGCGG 482
DB 420 GACTCCAAAGTCCCGGCTTCCCGGTGGCGGGAATGATGGGGCCACCGACGTCGCGG 479
QY 483 CGGGCTGACGCGGGTAGCCCAAGAAATCCCTCGGGGTAGGGCGGGTGGAATTTCTCT 542
DB 480 GCGGCTGACGCGGGTAGCCCAAGAAATCCCTCGGGGTAGGGCGGGTGGAATTTCTCT 539
QY 543 TTCTATACCATCATGSCAGTCTCTGCTGCTTCTCGTGGTGGGCGCGGSCCAATTCG 602
DB 540 TTCTATACCATCATGSCAGTCTCTGCTGCTTCTCGTGGTGGGCGCGGSCCAATTCG 599
QY 603 GCCCGGCCACCGCTGTGACGGAATGGGCAATATTTCCCTCACAATTTGCTGTCG 662
DB 600 GCCCGGCCACCGCTGTGACGGAATGGGCAATATTTCCCTCACAATTTGCTGTCG 659
QY 663 CCGGAAGACATCGGTTCTGCTGGAAGCGGATGCTGCTGGGCGCTGGGGTGACGCT 722
DB 660 CCGGAGACATCGGTTCTGCTGAGGGTGGATGCTGGGCGCTGGGGTGACGAT 719
QY 723 TGCACCGACGTTGTGGCCACTGATCAGCGGGTTTGGCTGTGCGGCCCTGGCAAGTCC 782
DB 720 TGCACGTACCAATGCTGGCCACTGATCAGCGGGTTTGGCTGTGCGGCCCTGGCAAGTCC 779
QY 783 GCGGCGGACGCTGTGGGAACTGGGAGCGCTGTACGGGCGCTGTGCGCTCGGCTTAC 842
DB 780 GCGGCGGAACTGTGGGAGCTGGGTAGCGCTATACGGGCGCTGTGCGCTCGGCTTAT 839
QY 843 GTAGCGGGATCTGGGTCTGGGCGAGTTTACTCCGGGGTCTCAGAGTTGGGTTCGG 902
DB 840 GTGGCTGGGATCTGGGCTGGGTGAGGTGTACTCGGGTGGCTTAACTGGGAGTTCGG 899
QY 903 TTGAGCGCGGGTGTACCTGATGCCCACTGAAATGTGCAAGTGAATGACGTTTAA 962
DB 900 TTGAGCGCGGGTGTACCGGTGCTTAACTGACGTGTGCAAGTGTGAGCTAAG 959
QY 963 TGGGGAAGTGAATTTGGAGATGGACTGAGCAGTTGGGCTTCAATTAAGTTTGGAA 1022
DB 960 TGGGGAAGTGAATTTGGAGATGGACTGAACAGCTGGGCTTCAACTACTGATTTGAA 1019
QY 1023 TACCTTTGGAAGTCCCAATTTGAATTTGGAGAGGAGTATGACGCTCACCCCTCTGTTG 1082
DB 1020 TACCTCTGGAAGTCCCAATTTGAATTTGGAGAGGCGTGATGAAGCCTGACCCCTTGTG 1079

QY 1083 GTTTGGGTGGCCGATTCGTTTTGCTGGAGCAACGGAATGTGATGGTTTTCTGCTGGTG 1142
DB 1080 GTTTGGGTGGCCGATTCGTTTTGCTGGAGCAACGGAATGTGATGGTTTTCTGCTGGTG 1139
QY 1143 ACGATGGCGGGGATGTTGCAAGGCGCCCGCTCCCGTTTGGGGTCCCGCCCTTTGAC 1202
DB 1140 ACGATGGCGGGGATGTTGCAAGGCGCCCGCTCCCGTTTGGGGTCAAGCCCTTTGAC 1199
QY 1203 TACGGGTGAAGTGGCAGTCACTGCTGCTGAGGCTAACGGGTGCGGTATTTCCACATGGG 1262
DB 1200 TACGGGTGAAGTGGCAGCCTGCTTTCAGGGGCAACGGTTGCGTTTTTCGACTGGG 1259
QY 1263 CAGAGGTGTGGGATCGAGGGAATGTCACGCTCTGTGTGACTGCCCAACGCGCCCTGG 1322
DB 1260 GAGAAGTGTGGGACCGTGGGAACGTTACGCTTCAGTGTGACTGCCCTAACGCGCCCTGG 1319
QY 1323 GTTTGGGTCCCGGCTTTTGGCAGCGGTTGGGTGGGGCGACCCCATACCCATTGGAGC 1382
DB 1320 GTGTGGTTGCCAGCCTTTTGCACAAGCAATGGCTGGGGTGACCCCATCATTATTGGAGC 1379
QY 1383 CACGACAAAACCAAGTGGCCCTATCATGCCCCCAATATGTTATGGTCTGTGTCGTA 1442
DB 1380 CACGGCAAAATCAGTGGCCCTTTTCATGCCCCCAGTATGTTATGGTCTGTCTACAGTC 1439
QY 1443 ACGTGCCTGTGGGTTCCGTCTTGTGTTTGCCTCGACCGCGGTGCTGTGATTCGAAGATC 1502
DB 1440 ACTTGCCTGTGGGTTCCGCTTCTTGGTTTGCCTCCACCACTGTCGCGACTCGAAGATA 1499
QY 1503 GATGTGGAGTTGGTGGCCGTTGGATCTGCCAGCTGCACCATAGCGGCTCTAGGGTCA 1562
DB 1500 GATGTGGAGTTAGTGGCAGTTGGCTTGCACCTGCGCATAGCGCGACTTTGGATCA 1559
QY 1563 TCGGATCGGACACGCGTGTGAGTCTCCAGTGGGGAGTCCCGTGGTAACTGTTAT 1622
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QY 1863 CGGATTCCTTCGAGTTCGCCCATTAACAACATGTCATGCGCGTAGGCAACGGAAGTG 1922
DB 1860 CGGATACCTTCATCTGTTGGTAGTGTCCACACAGCCCATTTAGCCTTCCACCGGGACG 1919
QY 1923 TTCGGGTCTTCCCGGAGTCCCGCCATTAACAACATGTCATGCGCGTAGGCAACGGAAGTG 1982
DB 1920 TTTGGGTCTTCCCGGGACCGCCCTCTCAACAACATGTCATGCTCTTTGGGGACCGAAGTG 1979
QY 1983 TCTGAGCATTTGGCGGAGCTGGGCTTACGGGGGGTGTCTACGAGGCTCTGGTTTCGAGG 2042
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DB 2100 GGCAGGCTGATGGTTTTATACATGTCCAGGGTCACTTGCAGGAGGTTGGATGCAAGCAAC 2159
QY 2163 TTCATCCCTCCTCCACGCTGGTCTCTTGGATTTTGTATTGTCTGCTCTATCTGATG 2222


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Db 8880 GGTGGGCTGAGTTGGCTAGGGGCTGTTGGCATCCAGGCTTACGGCTTCTCCCT 8939
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Oy 9363 GGTAAAGCTCGGCCCAAGCGGGTTCTACT 9395
|||||
Db 9360 GGAAGAGCTCGGCCCAAGCGGGTTCTACT 9392
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RESULT 7
AAT08812
ID AAT08812 standard; cdna; 9392 BP.
AC
AC AAT08812;
XX
XX 12-AUG-1996 (first entry)
XX
XX Hepatitis virus open reading frame sequence from clone 470-20-1.
DE
DE Hepatitis G virus; HGV; Flaviviridae; viral capsid protein; probe;
KW viral envelope protein; non-structural protein; RNA helicase; antibody;
KW chymotrypsin-like serine protease; RNA dependent RNA polymerase;
KW HGV genome; ds.
XX
XX Hepatitis G virus clone 470-20-1.
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FH Key Location/Qualifiers
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Qy	663	CC	GGAACACATCGGGTCTTCGCTGGAGCGGATGCCGTGTGGCCCTGGGGGTGCACGGTT	722
Db	660	CC	GAGACATCGGGTCTTCGCTGGAGGGTGGATGCCGTGTGGCCCTGGGGGTGCACGATT	719
Qy	723	TG	CACCACCGTTGCTGGCCACTGTATCAGCGGGTTTGGGTGTGCGGCCTGGCAAGTCC	782
Db	720	TG	CACTGACCAATGCTGGCCACTGTATCAGCGGGTTTGGCTGTGCGGCCTGGCAAGTCC	779
Qy	783	GC	GCCCCAGCTCGTTGGGAACTGGGAGCCGTGTACGGGCCCTTGTCCGGTTCGGCTTAC	842
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Qy	843	GT	ACCCGGATCTTGGGTCTGGGCGAGGTTTACTTCGGGGTTCCTGCAGTGTGGTGTGGC	902
Db	840	GT	GCTCGGATCTCGGGCTGGGTGAGTGTACTCGGGTCTCTAAACGGTGGGAGTCCGC	899
Qy	903	TT	GAGCGCCGGTCTACCTGTATGCCCAACCTGAAGTGTGCAGTAGAATGTGACGTTAAG	962
Db	900	TT	GACGCCCGGGTCTACCCGGTGCCTAACCTGACGTGTGCAGTCGGTGTGACCTAAG	959
Qy	963	TG	GGAAGTCAGTTTTGGAGTGGACTGAGCAGTTTGGCTCCAAATTACTGGATTTTGGAA	1022
Db	960	TG	GGAAGTCAGTTTTGGAGTGGACTGAACAGCTGGCTCCAACCTACTGGATTTTGGAA	1019
Qy	1023	TAC	CTTTGGAAATCCCATTTGAAATTTGGAGAGAGTATGAGCCGTGACCCCTCTGTTG	1082
Db	1020	TAC	CTCTGGAAAGTCCCATTTGATTTCTGGAGAGCGGTGAAGCCGTGACCCCTCTGTTG	1079
Qy	1083	GT	TTGGGTGGCCGATTTGCTTGGAGCAACGGAATGTCAATGGTTTCCCTGCTGGTG	1142
Db	1080	GT	TTGCTGGCCGATTTGCTGCTTGAGCAACGGAATGTCAATGGTCTTCTGTTGGTG	1139
Qy	1143	AC	GATGGCGGGATGTGTGAAGGCGCCCGCCCTCCGTTTGGGGTCCCGCCCTTTTGAC	1202
Db	1140	AC	GATGGCGGGATGTGTGAAGGCGCCCGCCCTCCGTTTGGGGTCAACGCGCCCTTTGAC	1199
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Qy	1263	GAG	AGGTGTGGGATCGAGGGAATGTACGCTCTTGTGTGACTGCCCAACGCCCTCTGG	1322
Db	1260	GAGA	AGGTGTGGGACCGTGGGAACGTTACGCTTACGTTGAGTGCCTTAACGCCCTCTGG	1319
Qy	1323	GT	TTGGTCCCGCCCTTTGCCAGGCGGTTGGTGGGGCGGACCCCATCACCCATTTGAGC	1382
Db	1320	GT	GTGTTGTCAGCCCTTTGCCAAGCAATCGCGCTGGGTGACCCCATCACTATTGGAGC	1379
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Qy	1443	AC	GTGCTGTGGGTTCCGTGTCTTGGTTTGCTCGACCGCGGTCTGTTTCGAAGATC	1502
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Qy	1503	GAT	GTTGGAGTTTGTGCGCGTTGATCTGCCAGCTGCACCATAGCCGCTCTAGGTCA	1562
Db	1500	GAT	GTTGGAGTTTGTGCGCGTTGATCTGCGACCTCTGCACCATAGCCGCACTTGGATCA	1559
Qy	1563	TC	GATCCGACACGGTGTGAGCTCTCCGAGTGGGAGTCCCGTGGGTAACTGTATT	1622
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QY	1743	GCTGTGCCCTTCGTCAACAGGACAACTCCCTTWCACCATAAAGGGGCCCTGGGCAACCAAG	1802
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QY	2163	TTCAATCCCTCCTCCAGCTGGTGTGCTCTTGGATTTGTGATTTGTCTGCTCTATCTGATG	2222
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QY	2223	AAGCTGGGCTGAGGCACGGTTGGTCCCGTTGATCTTGCTTCTGCTGTGGTGGGTGAAC	2282
DB	2220	AAGCTGGGCTGAGGCACGGTTGGTCCCGTGATCTTGCTGCTGCTATGGTGGGTGAAC	2279
QY	2283	CAGTTGGCGGTTCTAGGACTCCCGCTGTGGAGCTGCCGTGGCGGGTGAAGTTTTCGG	2342
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QY	2343	GGCCCTGCCTTCATGTGTGTTGGGCGCTCCCACTGTCCAGTATGATCTAGGCTTAGCA	2402
DB	2340	GGCCCTGCCCTGCTGCTGGAGTCTGGGACTCCCGCTGCTGCTGATGATATTTGGGTTGGCA	2399
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QY	2463	AAGCTCGCTCGGGGAGCTTCCCGCTGGCACTTTTTCATGGGATTTCCGCGACCCCGGG	2522
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DB 5520 GCGGGAGGTGGCGGCTGTGTTGGCCATTCGCCAAGGCTGATTCGTCGCGCGTGGCG 5579
QY 5583 GCTATGGGCTCTAGGAGCCCTCCATGGCTGCTGCGCTCTCTACTAGGGGCGCTGGG 5642
DB 5580 GCTACGGGCTTCAAGGAGCGCGGCTTGGCAGCGCGGCTTCCCTACCTGATGGGGTTG 5639
QY 5643 GCGCTCGGAGGAACGCGCAACCCGCTTAGCCTCCGCTCTCTACTAGGGGCGCTGGG 5702
DB 5640 GCGGTTGGAGGCAACCTCAGAGCGGCTGGCTCTGCGCTCTCTATTTGGGGGCTGTGA 5699
QY 5703 ACCGCTCTGGGACGCGCTGTGTTGGGTTAAACCATGGCGGGCGGCTTCATGGAAGTGT 5762
DB 5700 ACCGCTTGGGACCTCTGTCGTTGGCTTGAACCATGGCAGGTGCGTTTCATGGGGGGCG 5759
QY 5763 AGGCTCTCCGCTCTGCTACCACTTTACTTGGGGCGGCTGGGGGCTGGAGGCGCTG 5822
DB 5760 AGTGTCTCCGCTCTGCTGCTACCACTTTATTTGGGGCGGCTGGAGGTTGGAGGCTGT 5819
QY 5823 GTGAATCGGCTAGCCTGTCTTCGACTTATGGCGGGGAAACTATCATCAGAAGATCTG 5882
DB 5820 GTCAACGCGGAGCGCTAGTCTTTGACTTCATGCGCGGGAACCTTTCATCAGAAGATCTG 5879
QY 5883 TGTATGCCATCCAGTGTACCACTGCGGGGGCAGGACTTGGCGGGATTCGCGGCTCGGG 5942
DB 5880 TGTATGCCATCCGCTACTGACACCGGGGGCGGCGCTTGGCGGGATTCGCTCGGG 5939
QY 5943 TTGGTGTGTACTACCTAACACTCTGCACTTACCACTTGGTTGAACGCTGCTGCTGACT 6002
DB 5940 TTGGTTTTGTATCAGCTAACAACTCTGGCACTTACCACCTTGGTTGAACGCTGCTGACT 5999
QY 6003 ACATTCGCAAGTCTCTATCCCTGACGTTTACTTTTCAGCAGGCGCGATTTACTGTGAC 6062
DB 6000 ACGTTACCAAGTCTTCATGTATCCCGACAGTTACTTTTCAGCAAGTTGACTATTCGAC 6059
QY 6063 AAGGTCTAGCTGTGTCGACGCTTTCAGCCTTACCTGACACCGTGGTTGCCCTGGTCAAC 6122
DB 6060 AAGGTCTAGCCTGTGTCGCGGCTTACGCTTACCCGACAGTGGTTGCCCTGGTCAAC 6119
QY 6123 AGGAGCCTTAAGTGTAGGTTTACAGTGGGTAGCTGCGGACTTGGGAGTGGATC 6182
DB 6120 AGGAGCCTTAAGTGTAGGTTTACAGTGGGTATGCTGGGACCTGTTGGGAGTGGATC 6179
QY 6183 ATGCGTCAAGTGGCATGGTATGGCCAGACTTCGGGCGCTCTGCCCGTGGTGTATTA 6242
DB 6180 ATGCGCAAGTGGCGTGGTATGGCCAGACTCAGGGCGCTCTGCCCGTGGTGTCACTA 6239
QY 6243 CCTTATGCACTTCGCGGAGGGGTGGTCCGAGAAATGGTTGTGGACGCCCATGTTGAG 6302
DB 6240 CCTTGTGGCATTCGCGGAGGGGTGGTCCGGGAATGGTTGCTTACGGCTCATGTTGAG 6299
QY 6303 AGTGTGTCTTGTGGTGTGATCAGCGGTGATGTTTTGTAATGGGCAACTCAAGAT 6362
DB 6300 AGTGTGTCTCTGTGGCTGCGTGATCACTGTTGACGTTCTGAATGGGCAACTCAAGAA 6359

QY 6363 CCAGTTTACTCTACCAAGCTGTGAGGCACTATTGGATGGGACAGTCCCTGTGAACATG 6422
DB 6360 CCAGTTTACTCTACCAAGCTGTGCGGCACTATTGGATGGGACAGTCCCTGTGAACATG 6419
QY 6423 CTGGGCTATGGGAGACGTGCGCTTTGCTGCGCTCAGACACCCCGAAGTGTGACCATTC 6482
DB 6420 CTGGGTTACGGTGAACAGTCTGCTCTCTGCGCTCGACACCCCGAAGTGTGCGCTTC 6479
QY 6483 GGGACGCTCTGGTGGGCTGAGGTGTGTGACCCCTACCCACGTTGTGATCAGCGCAACA 6542
DB 6480 GGGACGCTCTGGTGGGCTGAGGTGTGTGACCCCTACCCACGTTGTGATCAGGAGGACC 6539
QY 6543 TCGCCCTACAACTGCTGCGCCAGCAAACTCTGTCGCGCTGCTGCTGAGCCCTATTAC 6602
DB 6540 TCGCCCTATAAGCTGCTGCGCCAGCAAACTCTATCGCTGCTGCTAGCTGAGCCCTACTAC 6599
QY 6603 TCGAGCGCATACCGGTCTCATGGGACGCGGAGCGCGGAGCGCTGCCATGCTATGGC 6662
DB 6600 GTCGAGCGCATTCGCGTCTCATGGGACGCGGAGCGCTGCTGCGCCCGCCATGTTATGGC 6659
QY 6663 CCTGGCAAGTGTCAACCATTTGACGGGGAACGCTACACCCCTCCGCTCAACTGCGGCTT 6722
DB 6660 CCTGGCAAGTGTACCATTTGACGGGAGCGCTACACCTTGCCCTCATCAACTGAGGCTC 6719
QY 6723 AGGAATGTGCGGCTCTGAGGTGTTCATCCGAGGTGTCCATTTGACATTTGGGACGAGACT 6782
DB 6720 AGGAATGTGCAACCTCTGAGGTTCATCCGAGGTGTCCATTTGACATTTGGGACGAGACT 6779
QY 6783 GAAGACTCAGAACTGACTGAGGCGGAGCTGCGCGCGGCGGCTGCTGCTCTCCAAAGCATC 6842
DB 6780 GAAGACTCAGAACTGACTGAGGCGGAGCTGCGCGCGGCGGCTGCTGCTCTCCAAAGCATC 6839
QY 6843 GAGAATGCTCGGAGAACTTCTGAACCTCATATAGATGTCTCATGTGAGATTTGCACTGACA 6902
DB 6840 GAGAATGCTCGGAGAACTTCTGAACCGCACTTGTATGATGATGAGGAGTGCATGAGTACA 6899
QY 6903 CCTCTCTTTTGGGAGTAGCCGAGAGATGCTGCTGTTGGGAGAGACATACACCCGCACT 6962
DB 6900 CCTCTCTTTTGGTAGTAGCCGAGAGATGCTGTTGGGAGAGACATACACCCGCACT 6959
QY 6963 CCATCCGACAGCTTATCTGCGTTACTGAGAGAGCCGAGATGAGAGAGCCCGTGGTG 7022
DB 6960 CCATCCGACAGCTTATCTGCGTTACTGAGAGAGCTCAGATGAGAGAGCCCGTGGTG 7019
QY 7023 TCTTCTCGCAGAGGATACCCGCTCTCTGACTCATTTGAGGTGCTATCCAAAGTCCGAG 7082
DB 7020 TCTTCTCGCAGAGGATACCCGCTCTCTGACTCATTTGAGGTGCTATCCAAAGTCCGAG 7079
QY 7083 ACAGCCGAAGGGAGGAGAAAGCGTCTTCAAGCTGGCTCTTTCCGCTACTAAAGCCTTTGTTT 7142
DB 7080 ACAGCCGAAGGGAGGAGAAAGTGTCTTCAAGCTGGCTCTTTCCGCTACTTAAAGCCTTTATTT 7139
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DB 7140 CCACAGAGGATGCCACAGAAAGCTTACCGTTAAGATGTCATGCTGCTGCTGTTGAAAGAGC 7199
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DB 7200 GTAAACAGCTCTCTTTTCAATGAGGATTTGACGCTGCTGAGTGGCAAGCCTGCTGAGATG 7259
QY 7263 GAATCCAGAACCATACAGCTTATTTGCAAGGTGCGGACTCCGCTTGAATTTGCAAGTTT 7322
DB 7260 GAATCCAGAACCATACAGCTTATTTGCAAGGTGCGGACTCCGCTTGAATTTGCAAGTTT 7319
QY 7323 GGTGCTTGTGGGCAATGAACCTTACCTTTGAATGTGACAAGTGTGAGGCTAGGCAAGAG 7382
DB 7320 GGTGCTTGTGGGCAATGAACCTTACCTTTGAATGTGACAAGTGTGAGGCTAGGCAAGAA 7379
QY 7383 ACCTTGGCTCTCTTCTTACATTTGCTGCGGCTGCCACTGACAGAGGGCCACTCGGCGC 7442
DB 7380 ACCTTGGCTCTCTTCTTACATTTGCTGAGTGGCGCTGCTGAGTGGCGGCGCGGCGC 7439
QY 7443 AAGCCCGCTTGTGTGAGGCGGCTTGGCTCTTCTGCTGCTGCGCCGACACCAAGGTGAT 7502

Db	8520	ATGTCGAGTCTAGTATAGTACACCGATGGCTTCGGCGATCGGTTACATCTCTCTTTATCTCT	8579
Qy	8583	TGGCATCTTATCACACGGTGGGTTCATCATCCCTCACGTGCTCACTCGCGCTTTTAGGGGT	8642
Db	8580	TGGCACCCATCACACGGTGGGTTCATCATCCCTCATGTGCTAACTGCGCATTCAGGGT	8639
Qy	8643	GGTGGCACACCGTCTCATCTCTGTGGTGCCAGGTACATGGTAATTACTACAAGTTTCCA	8702
Db	8640	GGAGGCACACCGTCTCATCCGGTTTGGTGCCAGGTGCATGGTAACTACTACAAGTTTCCA	8699
Qy	8703	CTGGACAAATCGCTTAACATCATCGTGGCCCTCCACGGACACAGCAGCTTCAGGGTTACC	8762
Db	8700	CTGGACAAATCGCTTAACATCATCGTGGCCCTCCACGGACACAGCAGCTTCAGGGTTACC	8759
Qy	8763	GCAGACAACTAAGACAAAAATGGAGGCTGCGAAGGTGCTGAGGAGCCTCAAGCTCCCT	8822
Db	8760	GCAGACAACTAAAACAAAGATGGAGGCTGGTAAGGTCTGAGCGACCTCAAGCTCCCT	8819
Qy	8823	GGCCTAGCAGTCCACCGGAAGAGCGGGGCATTTGCAAGCGGTATGCTCCCGTCCGCG	8882
Db	8820	GGCTTACAGTCCACCAGAAAGAGCGGGGGCTTTGCCAACACGCATGCTCCGTCGCGC	8879
Qy	8883	GGTTGGGCTCAGTTGGCTAGGGGCTGTGTTGGCGTCCAGGCTGCGGCTTCCCGCTCGG	8942
Db	8880	GGTTGGGCTCAGTTGGCTAGGGGCTGTGTTGGCATCCAGGCTACGGCTTCTCTCCCT	8939
Qy	8943	GAGATTCTCGTATCCCGGGGTTTCCCTTTTCCCGCCCTATATGGGGGTGGTTTCA	9002
Db	8940	GAGATTCTCGTATCCCGGGGTTTCCCTTCTCTTCCCGCCCTATATGGGGGTGGTACAT	8999
Qy	9003	CAATTGGATTTCACAGCCAGAGGAGTCGCTGGCGGTGGTTGGGGTCTTTAGCCCTGCTC	9062
Db	9000	CAATTGGATTTCACAGCCAGAGGAGTCGCTGGCGGTGGTTGGGGTCTTTAGCCCTGCTC	9059
Qy	9063	ATCGTAGCCCTCTTGGGTGAACATAATTTCATCTGTTGGGGCAAGGTCGCGTGAATGTC	9122
Db	9060	ATCGTAGCCCTCTTGGGTGAACATAATTTCATCTGTTGGGGCAAGGTCGCGTGAATGTC	9119
Qy	9123	ATCACTGGAGAGGTTCCCGCCCTCCCGCCGCCAGGGGTCTCCCGCTGGGTAAAAAGG	9182
Db	9120	ATCACCGAGAGGTTCCCGCCCTCCCGCCGCCAGGGGTCTCCCGCTGGGTAAAAAGG	9179
Qy	9183	CCGGGCTTGGGAGGATGGTGTGTTACTTAACCCCTTGGAGGGTCAAGCCGTGATGTGC	9242
Db	9180	CCGGGCTTGGGAGGATGGTGTGTTACTTAACCCCTTGGAGGGTCAAGCCGTGATGTGC	9239
Qy	9243	TAATGCATCTCCACTTTCGGGTGGCGGTTCGCTACCTTATAGCGTAAATCCGTGACTACGGC	9302
Db	9240	TAATGCATCTCCACTTTCGGGTGGCGGTTCGCTACCTTATAGCGTAAATCCGTGACTACGGC	9299
Qy	9303	TGCTCGCAGAGCCCTCCCGGATGGGGCACAGTGCACTGTGATCTGAAGGGGTGCACCCC	9362
Db	9300	TGCTCGCAGAGCCCTCCCGGATGGGGCACAGTGCACTGTGATCTGAAGGGGTGCACCCC	9359
Qy	9363	GGTAAGAGCTCGGCCCAAGGGCCGGT	9389
Db	9360	GGGAAGAGCTCGGCCCAAGGGCCGGT	9386
RESULT 9			
AAT94168			
ID	AAT94168 standard; cdna; 9391 bp.		
XX			
AC	AAT94168;		
XX	01-MAY-1998 (first entry)		

RESULT 9	
AAT94168	
ID	AAT94168 standard; cDNA: 9391 BP
XX	
AC	AAT94168;
XX	
DT	01-MAY-1998 (first entry)
XX	
DE	Hepatitis G virus PNF-2161 genome
XX	
KW	HGV; protease; fusion protein; ds
KW	protease; PNF-2161 genome; ds.
XX	
OS	Hepatitis G virus.

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XX FH Key Location/Qualifiers
XX FT CDS 459..9080
XX FT /*tag= a
XX PN WO9740168-Al.
XX PD 30-OCT-1997.
XX PF 24-APR-1997; 97WO-US06944.
XX PP 24-APR-1996; 96US-0638911.
XX PR (GENE-) GENELABS TECHNOLOGIES INC.
XX PA Belyaev AS, Chong SM;
XX PI WPI; 1997-535852/49.
XX DR P-PSDB; AAW34983.
XX PT Hepatitis G virus protease - useful to develop products to study,
XX PS diagnose and treat hepatitis G virus infection
XX PS Example 1; Pages 26-38; 115pp; English.
XX CC The present sequence was used in the development of a composition
XX CC comprising, or a polynucleotide encoding an isolated hepatitis G
XX CC virus (HGV) protease, or a fusion protein comprising a suitable
XX CC fusion partner fused to a proteolytic polypeptide derived from HGV.
XX CC The products can be used to diagnose and treat HGV infection.
XX SQ Sequence 9391 BP; 1694 A; 2551 C; 2998 G; 2148 T; 0 other;

Query Match 84.9%; Score 7971.8; DB 18; Length 9391;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 8509; Conservative 0; Mismatches 877; Indels 1; Gaps 1;

QY 3 ACGTGGGGGGTGTATCCCGCCCGCCGCACTGGGTGCAAGCCCAATAAACCGAGCCCT 62
DB 1 ACGTGGGGAGTTGATCCCGCCCGCCGCACTGGGTGCAAGCCCAATAAACCGAGCCCT 60
QY 63 ATCTAAGTAGAGCAATGACTCGGCGCCGACTCGGCGACCCGCCCAAAAGGTGGTGGATG 122
DB 61 ATCTAAGTAGAGCAATGACTCGGCGCCGACTCGGCGACCCGCCCAAAAGGTGGTGGATG 120
QY 123 GTGGTGACAGGTTGGTAGGTGCTAAATCCCGTCACTCTGTAGCCACTATAGTGGGT 182
DB 121 GTGATGACAGGTTGGTAGGTGCTAAATCCCGTCACTCTGTAGCCACTATAGTGGGT 180
QY 183 CTTAAGAGAGGTCAAGACTCCTCTTGTGCTCGCGAGACCGCGACGTCACAGGT 242
DB 181 CTTAAGAGAGGTCAAGACTCCTCTTGTGCTCGCGAGACCGCGACGTCACAGGT 240
QY 243 GCTGGCCCTACCGGTGTGAATAAGGSCCGAGCTCAGGCTCGTGTAAACCGAGCCCGT 302
DB 241 GTTGGCCCTACCGGTGGGAATAAGGSCCGAGCTCAGGCTCGTGTAAACCGAGCCCGT 300
QY 303 CACCCACTGGGCAACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 362
DB 301 TACCCACCTGGGCAACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 360
QY 363 ACCAATAGGTTTATCCGGCGAGTTGACAAGGACAGTGGGGCGCGGGGTATGGGGAAG 422
DB 361 ACCAATAGGCGTAGCGCGGAGTTGACAAGGACAGTGGGGCGCGGGGCT-TGGAGAGG 419
QY 423 GACCCCAACCCCTGCCCTTCCCGGTGGCGGGAATGATGGGGCACCCAGCTCCGG 482
DB 420 GACTCCAAAGTCCCGCCCTTCCCGGTGGCGGGAATGATGGGGCACCCAGCTCCGG 479
QY 483 GCGGGCTGACGCGGGGTAGCCCAAGAAATCCTTCGGGTGAGGGCGGGGTGCTCTTT 542
DB 480 GCGGGCTGACGCGGGGTAGCCCAAGAAATCCTTCGGGTGAGGGCGGGGTGCTCTTT 539
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QY 543 TTCTATACCATCATGCGAGTCTTCTGCTCCTCTCTGCTGTTGAGCGCGGGCCATTCTG 602
DB 540 TTCTATACCATCATGCGAGTCTTCTGCTCCTCTCTGCTGTTGAGCGCGGGCCATTCTG 599
QY 603 GCCCGGCCACCCACGCTTGTGAGCAATGGCAATATTTCTCTCAAAATGCTGTGCC 662
DB 600 GCCCGGCCACCCACGCTTGTGAGCAATGGCAATATTTCTCTCAAAATGCTGTGCC 659
QY 663 CCGGAAGACATCGGTTCTGCTGGAAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 722
DB 660 CCGGAGGACATCGGTTCTGCTGAGGTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 719
QY 723 TGCACCGACCGTTGCTGCGCACTGATACAGGGGGTTTGGCTGTGCGGCTGSCAAGTCC 782
DB 720 TGCACCTGACCAATGCTGCGCACTGATACAGCGGGTTTGGCTGTGCGGCTGSCAAGTCC 779
QY 783 GCGGGCCAGCTCGTTGGGGAACCTGGGAGCCCTGTACGGGCCCTTGTGCTGCTGCTGCT 842
DB 780 GCGGGCCAACTGCTGGGGAGCTGGGTAGCTATACGGGCCCTGTGCTGCTGCTGCTGCT 839
QY 843 GTAGCGGGATCCTGGTCTGGCGAGGTTTACTCCGGGGTCTGACACTTGTGCTGCTG 902
DB 840 GTGGCTGGGATCCTGGGCTGGGTGAGGTGTACTCGGGGTCTCTAACGGTGGGAGTCCG 899
QY 903 TTGAGCGCGCGGTCTTACCTGATGCCCAACCTGAAGTGTGCAGTAGAATGTGACGTTAAG 962
DB 900 TTGAGCGCGCGGTCTTACCGGTGCTTAACCTGACGTGTGCAGTGTGCTGCTGCTGCTG 959
QY 963 TGGGAAGTGAAGTTTGGAGATGGACTGAGCAGTGTGGCCCTCCAATTTACTTGGGAA 1022
DB 960 TGGGAAGTGAAGTTTGGAGATGGACTGAGCAGTGTGGCCCTCCAATTTACTTGGGAA 1019
QY 1023 TACCTTTGAAAGTCCCAATTTTGGAGAGGAGTGTGACGCTGACGCTGACCCCTCTGTTG 1082
DB 1020 TACCTCTGGAAGTCCCAATTTGATTTCTGGAGAGGCTGATAAGCCTGACCCCTTGTG 1079
QY 1083 GTTGTGGTGGCGCGATTGCTTTGTGGAGCAACGATTGTCTATGTTTCTCTGCTGGTG 1142
DB 1080 GTTGTGGTGGCGCGATTGCTTTGTGGAGCAACGATTGTCTATGTTTCTCTGCTGGTG 1139
QY 1143 AGTATGGCGGGATGTTGCAAGCGCCCGCCCTCGTGTGTTGGGGTCCGCGCCCTTTGAC 1202
DB 1140 AGTATGGCGGGATGTTGCAAGCGCCCGCCCTCGTGTGTTGGGGTCCGCGCCCTTTGAC 1199
QY 1203 TACGGTTGAAGTGGCAGTATGCTCTCGAGGGCTAAAGGGTCCGCTATTTCCCACTGG 1262
DB 1200 TACGGTTGAAGTGGCAGTATGCTCTTGCAGGGCAACGGTTCGCGTTTTTCGACTGG 1259
QY 1263 GAGAGGTGTGGATCGAGGGAATGTCAGGCTTGTGTGACTGCCCAACGCGCCCTGG 1322
DB 1260 GAGAGGTGTGGATCGAGGGAATGTCAGGCTTGTGTGACTGCCCAACGCGCCCTGG 1319
QY 1323 GTTGTGGTCCCGCCCTTTTGCAGGCGGTGGTGGGGGACCCCATCATCCCATTTGGAGC 1382
DB 1320 GTGTGGTTGCCAGCTTTTGCCAAGCAATCGGCTGGGGTGACCCCATCACTTATTGGAGC 1379
QY 1383 CACGACAAACACGATGGGCCCTATCATCCCCCAATATGTCTATGGGTCTGTGCTCCGTA 1442
DB 1380 CACGACAAACACGATGGGCCCTTTCATCCCCCAATATGTCTATGGGTCTGTGCTCCGTA 1439
QY 1443 AGCTGCTGCTGGGTTCCTGCTTGTGTTGCTTGCACCGGGGTGCTGATTCGAAGATC 1502
DB 1440 ACTTGGTGTGGGTTCCTGCTTGTGTTGCTTGCACAGTGGTCCGACTCGAAGATA 1499
QY 1503 GATGTGTGAGTTTGGTGGCGGTGGATGTCAGCTGTCACCATAGCCGCTCTAGGGTCA 1562
DB 1500 GATGTGTGAGTTTGGTGGCGGTGGATGTCAGCTGTCACCATAGCCGCTCTAGGGTCA 1559
QY 1563 TCGGATCGGACACGATGGTGTGAGCTCTCCGAGTGGGGAGTCCCGTGCCTTAAGTAT 1622
DB 1560 TCGGATCGGACACGATGGTGTGAGCTCTCCGAGTGGGGAGTCCCGTGCCTTAAGTAT 1619
QY 1623 CTGGACCGTGGCTGCTTCTATGTGCGGAGTGTGCTGCGGGAGTGTGCTGCGGCAACCGGG 1682
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Db 6000 ACCTTACCAAGGCTTCATGTATCCCGACAGGTTACTTTTCAGCAAGTTGACTATTGCGAC 6059
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Db 6060 AAGGTCTCAGCGGTGCTCCGCGGCTGAGGCTCACCCGACAGGTTGCTCCCTGGTCAAC 6119
Qy 6123 AGGAGCCTAAGGTGGATGAGGTTTCAGGTGGGTGAGTCTCTGGGACTTGTGGGAGTGATC 6182
Db 6120 AGGAGCCTAAGGTGGATGAGGTTTCAGGTGGGTGAGTCTCTGGGACTTGTGGGAGTGATC 6179
Qy 6183 ATGCGTCAAGTGCACATGATGAGGCTTCAGGCTTCGCGCCCTCTCGCCCGTGGTCAATTA 6242
Db 6180 ATGCGCAAGTGCAGGTGGTCAATGCGCAGACTCAGGCGCCCTCTCGCCCGTGGTCACTA 6239
Qy 6243 CCCTTATGGCACTCGCGGAGGGTGTCCGGAGAAATGTTGTTGGACGGCCATGTTTGGAG 6302
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Qy 6303 AGTCGTTGCTTGTGTTGCTGATCACCCTGGTATGTTTGAATGGGCAACTCAAGAT 6362
Db 6300 AGTCGCTGCCCTCTGTGCTGCTGATCAGTGTGACGTTCTGAATGGCAACTCAAGAA 6359
Qy 6363 CCAGTTTACTCTACCAAGCTGTGAGGCAATTAATGGATGGGACAGTCCCTGTGAACATG 6422
Db 6360 CCAGTTTACTCTACCAAGCTGTGCGGCACTAATTTGGATGGGACTGTCCCTGTGAACATG 6419
Qy 6423 CTGGGCTATGCGGAGAGCTGCGCTTCTGCTGCTCAGACACCCGGAAGTGGTACCATTTC 6482
Db 6420 CTGGGTTACGTTGAACGTCGCTCTCTGCTGCTCAGACACCCGGAAGTGGTCCCTTC 6479
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Db 6660 CCTGGCAAGTGTACCAATTCAGCGGGAAGCGCTTACACCTTCGCGCTCACTCAACTGAGGCTC 6719
Qy 6723 AGGAATGTGGCGCCCTCTGAGGTGTATCGAGGTGTCCATTTGACATTTGGACCGGAGACT 6782
Db 6720 AGGAATGTGGCACCCCTCTGAGGTTTTCATCGAGGTGTCCATTTGACATTTGGACCGGAGACT 6779
Qy 6783 GAAGACTCAGAACTGACTGAGCGCGACTGCGCGCGCGGCTGCGAGCCCTTCAGGCTATC 6842
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Qy 6843 GAGAATGTGCGAGAATCTTGAACCTCACATAGATGTCAATCATGGAAGATTCAGATACA 6902
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Qy 7083 ACACCGAGGGGAGGAAGGCTTCAAGTGGCTCTTCCCGTACTTAAAGCCCTGTTT 7142
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Qy 7263 GAAATCCAGAACCATACAGCCTATTTGACAAGTGGCGACTCCGCTTGAATTTGACAGTTT 7322
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Qy 7323 GGGTGTGTGGGCAATGAACCTTACCTTTTGAATGTGACAAGTGTGAGGTAGGCAAGAG 7382
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Qy 7383 ACCTTGGCTTCTCTTCTTACATTTGCTTGGGTGGCACTGAGAGGGCCACTCCGGCC 7442
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Qy 7443 AAGCCCTCTGTGTGAGCGCGTGGCTCTGCTGTGGCGGACACACCAAGGCTGTAT 7502
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Qy 7503 GTACCAACCCGCAATTTGGGAGAAAGATTGACAAGGTTTACCTTCTGCGCTGCCCT 7562
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Qy 7683 ATGGCTGGGATCTTAAGTGTGCTCAAGGACTCCGCCACCCCTCGGGGGAAGATGGCT 7742
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Qy 7743 GTCATGACCGCTTCCAGGAGATCTTTGAAGGAGCGCACTCCCTTTACTCTTACTCTGTG 7802
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Qy 7923 AAGCGGTGTGGGGGGGCTTACGCTTCCAGTACACCCCAATACAGCAATTAGGAG 7982
Db 7920 AAGCGGTGTGGGGGGGCTTACGCTTCCAGTACACCCCAATACAGCAATTAGGAG 7979
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Db 7980 ATGCTCAAGTGTGGGAGTCTAAGAGACCCCTTGGCCCATCTGTGTGAGCGCCACCTGC 8039
Qy 8043 TTCGACAGTAGCTAAGTGAAGAGGAGCTGGCGCTGGAGACAGAGCTTTATGCGCTGGCT 8102
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Qy 8103 TCAGACCATCCGAATGGGTGCTGCCCTGGGAAATACTATGCTCTGGCAATGGTA 8162
Db 8100 TCTGACCATCCGAATGGGTGCGGCACTTGGGAAATACTATGCTCTGAGCGCCATGGTC 8159
Qy 8163 ACCCGGAGGGGTGCGAGTGGGTGAGAGTATTTGATAGTCTCAGGGGCTTGTGACCACC 8222
Db 8160 ACCCGGAAGGGGTGCGGCTGCGGTGAGAGTATTTGAGAGTCTCCTGGGTGCTTAAACACT 8219
|||||

Qy	8223	AGTGCAGCAACTGCTTGACTTGCTATATATCAAGGTGAAGCCGCCTGTGAGAGGGTGGGG	8282
Db	8220	AGCGCAGCAACTGCTTGACTTGCTATATATCAAGGTGAAGCTGCTGTGAGAGAGTGGG	8279
Qy	8283	CTCAAAAATGCTTCGCTCCTCATCGCTCGCATGACTGTTTGTGATCATATGCGAACGGCCT	8342
Db	8280	CTCAAAAATGCTTCGCTCCTCATACCGCGGATGACTGCTTGTATCATATGTGACGCGCCA	8339
Qy	8343	GTGTGCGATCTTAGCGACGCTTTTGGCGAGAGCCCTTGGCGAGCTACGGGTACGCATGCGAG	8402
Db	8340	GTGTGCGACCCAAGCGACGCTTTGGCGAGAGCCCTAGCGAGCTATGGTACGCGTGGCAG	8399
Qy	8403	CCCTTCGTATCATGTCATCTAGACAGCGGCCCTTCCTGCTCCACTTGGCTAGCTGAGTGC	8462
Db	8400	CCCTCATATCATGTCATCATTTGGACAGCGGCCCTTCTGCTCCACTTGGCTAGCTGAGTGC	8459
Qy	8463	AATGTCAGATGGGAACGCCATTTCTTCTGACACCGACTTTTCGGAGGCCCTTCGCTGCTCG	8522
Db	8460	AATGTCAGATGGGAGCGCCATTTCTTCTGACACCGACTTTTCGGAGGCCCTTCGCTGCTCG	8519
Qy	8523	ATGTCGAGCGAGTACAGTGACCAATATGGCTTCGGCCATCGGTTACATCTCCTATACCCCT	8582
Db	8520	ATGTCAGTGAATAGTAGTGACCCGATGGCTTCGGCGATCGGTTACATCTCCTTTATCCT	8579
Qy	8583	TGCACTCCTATCACACGGTGGGTATCATCCCTCACGTGCTCACCTCGCGGTTTAGGGGT	8642
Db	8580	TGCAACCCATCACACGGTGGGTATCATCCCTCATGTGCTTAACGTGCGCATTCAGGGGT	8639
Qy	8643	GGTGGCACACCGTCTGATCCTGTGTGGTGCAGGTACATGTTAATTACTACAAGTTTCCA	8702
Db	8640	GGAGCAGACCGTCTGATCCGGTTTGGTGCCAGGTGCATGTACTACTACAGTTTCCA	8699
Qy	8703	CTGGCAAACTGCCTTAACATCATCTGCGCCCTCCACGGACAGACGGTTGAGGGTTACC	8762
Db	8700	CTGGCAAACTGCCTAACATCATCTGCGCCCTCCACGGACAGACGGTTGAGGGTTACC	8759
Qy	8763	GCAGACACAACATAAGCAAAAATGACGGCTGGCAGGTGCTGACGGACCTCAAGCTCCCT	8822
Db	8760	GCAGACACAACATAAACAAGATGAGGCTGGTAAGTTCTGACGACCTCAAGCTCCCT	8819
Qy	8823	GGCCTAGCAGTCCACCGGAAGACCGGGGCATTGGCAACCGCTATGCTCCGCTCGCGC	8882
Db	8820	GGCTTAGCAGTCCACCGGAAGACCGGGGCATTGGCAACACCATGCTCCGCTCGCGC	8879
Qy	8883	GGTTGGCTGAGTTGGCTAGGGGGCTGTGTGGCGTCCAGGCCTGCGGCTTCCCCCTCG	8942
Db	8880	GGTTGGGCTGAGTTGGCTAGGGGGCTGTGTGGCATCCAGGCCTACGGCTTCCTCCCT	8939
Qy	8943	GAGATTGCTGGTATCCCGGGGTTTCCCTTTCCTCCCGCCCTATATGGGGGTGGTTCAT	9002
Db	8940	GAGATTGCTGGTATCCCGGGGGTTTCCCTCTCTCCCGCCCTATATGGGGGTGGTACAT	8999
Qy	9003	CAATTGGATTTACAAAGCCAGAGTAGTCCGCTGGGGTGGTTGGGGTCTTTAGCCCTGCTC	9062
Db	9000	CAATTGGATTTACAAAGCCAGAGGAGTCCGCTGGGGTGGTTGGGGTCTTTAGCCCTGCTC	9059
Qy	9063	ATCGTAGCCCTCTTCGGGTGAACATAAATCATCTGTTCGGCGCAAGTCCGGTGACTGATC	9122
Db	9060	ATCGTAGCCCTCTTCGGGTGAACATAAATCATCTGTTCGGCGCAAGTCTGGTGACTGATC	9119
Qy	9123	ATCACTTGGAGGAGTTCCCGCCCTCCCGCCCGCAGGGGTCTCCCGCTGGGTAAAAAGG	9182
Db	9120	ATACCGGAGGAGTTCCCGCCCTCCCGCCCGCAGGGGTCTCCCGCTGGGTAAAAAGG	9179
Qy	9183	CCCGCCCTTGGGAGCATGGTGGTTTACTAACCCCTTGGCAGGGGTCAAAGCCTGATGGTGC	9242
Db	9180	CCCGCCCTTGGGAGCATGGTGGTTTACTAACCCCTTGGCAGGGGTCAAAGCCTGATGGTGC	9239
Qy	9243	TAATGACTGCCACTTCGCTGGCGGGTGCCTACCTTATAGCGTAAATCCGTGACTACGGGC	9302
Db	9240	TAATGACTGCCACTTCGCTGGCGGGTGCCTACCTTATAGCGTAAATCCGTGACTACGGGC	9299

Qy	9303	TGCTCGCAGAGCCCTCCCCGATGGGCACAGTCGTACTGTGAAGGGTGCACCCC	9362
Dd	9300	TGCTCGCAGAGCCCTCCCCGATGGGCACAGTCGTACTGTGAAGGGTGCACCCC	9359
Qy	9363	GGTAAAGAGCTCGGCCCAAGGCGGGT	9389.
Dd	9360	GGGAAGAAGCTCGGCCCGAAGCGCGTT	9386
RESULT	10		
AAV66279	ID	AAV66279 standard; cDNA; 9327 BP.	
XX	XX	AAV66279;	
XX	XX	23-DEC-1998 (first entry)	
DE	XX	Recombinant HGV sequence designated 3Z-HGV94-6.	
KW	XX	PNF2161 sera; antigen; immunoreaction screening;	
KW	XX	Non-A Non-B Non-C Non-D Non-E Hepatitis virus; HGV;	
KX	XX	anti-HGV antibody; vaccine; 3Z-HGV9461; ds.	
OS	XX	Synthetic.	
OS	XX	Hepatitis G virus.	
PN	XX	US5824507-A.	
PD	XX	20-OCT-1998.	
PF	XX	19-MAY-1995; 95US-0444733.	
PR	XX	19-MAY-1995; 95US-0444733.	
PR	XX	20-MAY-1994; 94US-0246985.	
PR	XX	03-AUG-1994; 94US-0285543.	
PR	XX	03-AUG-1994; 94US-0285543.	
PR	XX	26-OCT-1994; 94US-0329729.	
PR	XX	23-NOV-1994; 94US-0344271.	
PR	XX	16-DEC-1994; 94US-0357509.	
PA	XX	15-FEB-1995; 95US-0389886.	
PI	XX	(GENE-) GENELABS TECHNOLOGIES INC.	
PL	XX	Fry KE, Kim JP, Linnen JM, Wages J, Young LM;	
PP	XX	WPI; 1998-582553/49.	
PT	XX	Polypeptide antigens hepatitis G virus - useful as vaccines against the virus and raising antibodies for use in immuno-testing for the virus	
PS	XX	Example 18; Columns 337-346; 206pp; English.	
SC	XX	The present sequence represents a recombinant Hepatitis G virus (HGV) sequence derived from PNF2161, and designated 3Z-HGV9461. The specification describes HGV antigen clones isolated from PNF2161 sera. This sera is obtained from a patient suffering from Non-A Non-B Non-C Non-D Non-E Hepatitis virus, also known as Hepatitis G virus (HGV). HGV antigens can be used in immunoreaction screening for presence of anti-HGV specific antibodies, especially in patient sera, e.g. enzyme linked immunoassay (ELISA). They can also be used as vaccines, and to raise the polyclonal and monoclonal antibodies.	
SQ	XX	Sequence 9327 BP; 1682 A; 2532 C; 2984 G; 2129 T; 0 other;	

Db	2220	TGCTGCTATGGTGGGTGAACCAAGCTGGCGAGTCCTTAGGGGCTGCCGGGCTGTGGGAAGCCG	2279
Qy	2320	CCGTGGCGGGTGAAGTTTTTGGGGGGCCCTGCCCTGTCTATGGTGTGGGCGCTTCCCACTG	2379
Db	2280	CCGTGGCAGGTGAGGTCTTTCGCGGGCCCTGCCCTGTCTCTGCTGTGGACTCCCGGTG	2339
Qy	2380	TCAGTATGATACTAGTCTAGCAAAACCTTGGTGTGTGTACTTTCGGTGTGATGGGCCCTCAGC	2439
Db	2340	TCAGTATGATATTGGGTGTGGCAAACTTGGTGTGTACTTTAGATGTGGGACCCCAAC	2399
Qy	2440	GCCTCATGTTCCCTCGTGTGTGGAAGCTCGCTCGGGGAGCTTTCCTCGCTGSCACTTTTGA	2499
Db	2400	GCCTGATGTTCCCTGTTGTGTGGAAGCTTGTCTCGGGGAGCTTTCCTCGCTGGCCCTCTTGA	2459
Qy	2500	TGGGGATTTCGGCGACCCCGGGCGCACCTCTGTGTCTCGGGCCGAGTCTTGTCTCGATG	2559
Db	2460	TGGGGATTTCGGCGACCCCGGGCGCACCTCAGTCTCTCGGGCGAGTCTTGTCTTCGATG	2519
Qy	2560	TCACATTGAGGTGGACACTTCGGGTGTGGGCTGGGTGGTGGCCAGACGTTGGTGGCTTGGG	2619
Db	2520	CTACATTGAGGTGGACACTTCGGGTGTGGGCTGGGTGGTGGCCAAATGTGGTAGCTTTGGG	2579
Qy	2620	CCATTAGCGTTCCTAGACTCAATGAGCGCAGGGGGGTGGAAGCAAGGCGCGTGATCTATA	2679
Db	2580	CCATTGGCTCTCAGACTCGATGAGCGCAGGGGGGTGGAGGCACAAAGCCGTGATCTATA	2639
Qy	2680	GGACGTGGTGTAAAGGTTACCAAGGTGTGCGCCAGAGAGGGTGTGCGAGCCCGCTCGGGG	2739
Db	2640	GGACGTGGTGTAAAGGTTACCAAGGTAATCCGTCAAAAGGTTGGTGGAGGAGCCCGCTCGGG	2699
Qy	2740	AGGGGGCTCTACCAAGCTTCTGACGTTTCGGCTGTGTGTGGCCCTCATACATCTGGCCGG	2799
Db	2700	AGGGGGGGCTGCGCAACCCCTGACCTTTGCCGTGGTGTGGCCCTGATCTCTGGCCAG	2759
Qy	2800	ATGCTGTGATGATGGTGGTGGCTTGGTCTCTCTCTCGGCCCTGTGTGAGCAGCTGG	2859
Db	2760	ATGCTGTGATGATGGTGGTGGTGGCTTGGTCTCTCTTGGGCCCTGTGTGACGCGCTGG	2819
Qy	2860	ACTGGGCCCTGGAGGAGCTCTCGTCTCCGGCCCTCTGTACGCGCAGCTGGCAGCGGTGG	2919
Db	2820	ATTGGGCCCTGGAGGAGATCTTGGTGTCCGGCCCTCGCTCGCGCGTGTGGCTCGGGGTGG	2879
Qy	2920	TTGAGTGTGTGTATGGCGGGGAGAGGGCCACACCATCCGACTGGTCTCCAAAGATGT	2979
Db	2880	TTGAGTGTGTGTATGGCGGGTGAAGAGGCCAACCGTCCCGCTGGCTGTCTCCAAGATGT	2939
Qy	2980	GCACAAGAGGGCTACCTGTTTGTACCATGAGGCTCTTCTCGCGCGCTGTGTCAAGAGC	3039
Db	2940	GTGCGAGAGAGGCTTATTGTTTGTGATCATATGGGCTCAATTTTCGCGTGTGTCAAGGAGC	2999
Qy	3040	GCTTGTGTGAATGGGACGGGCTTTGGAGCCCTTGTCAATTCACCTAGACAGGACTGTGCGA	3099
Db	3000	GCCTGTGTGAATGGGACGGGCTTGTGAACCTCTGTCAATTCACCTAGACAGGACTGTGCGA	3059
Qy	3100	TCATCAGAGATGCCGCGAGGACCCCTGTCTCTCGGACAGTGGGTCTATGGTTTACCCGTGG	3159
Db	3060	TCATACGGGATGCCGCGAGGACTTTGTCTCTCGGGCAATGCGTCTATGGGTTTACCCGTGG	3119
Qy	3160	TAGCAGCGCGGTGATGAGGTTCATCAGCGGCTCTTTCAGGATGTGAACTATTGGCCTC	3219
Db	3120	TTGCGGCGCGGTGATGAGGTTCATCAGCGGCTCTCCAGGATGTGAACTATTGGCCTC	3179
Qy	3220	CCGGTTTGTCCGAGCTGCACCAAGTTGTATCCGTCGTCGGGAAAGGGCTTCTCTGGGGG	3279
Db	3180	CCGGTTTGTTCGACCGCGCCTGTTGTATCCGACGGTGGGAAAGGGCTTCTTGGGGG	3239
Qy	3280	TCACGAAGGCGCTTTCAGAGGTAGGGATCTCTGACTTACATCCAGGGAAGCTCATGTGT	3339
Db	3240	TCACAAAGGCTGCTTTCAGAGGTTCGGATCTCTGACTTACATCCAGGGAAGCTCATGTGT	3299
Qy	3340	TGGGAGCGGTACGTCACGAAGCATGGGCACATGCTGAATGGGCTGCTGTTCACAACTT	3399
Db	3300	TGGGAGCGGTACGTCGGAAGCATGGGAACATGCTTCAAGCGGCTGCTGTTCACGACCT	3359

Db 6600 GTGGCCCGCCATGGTCTATATGGCCCTTGGCCAAAGTTTACCATTTGACGGGGAGCGCTACA 6659
QY 6700 CCTTCCGCATCAACTGGGGCTTAGGAATGTGGCCCTCTGAGGTGTGTCATCCGAGGTGT 6759
Db 6660 CCTTCCGCATCAACTGAGGCTCAGGAATGTGGCCCTCTGAGGTTCATCCGAGGTGT 6719
QY 6760 CCATTGACATTTGGGACGAGACTGAAGACTCAGAATCTGACTGAGCCGACCTGCGCCGG 6819
Db 6720 CCATTGACATTTGGGACGAGACTGAGACTCAGAATCTGACTGAGCCGACCTGCGCCGG 6779
QY 6820 CGGCTGCAGCCCTTCAGGCTATCGAGAATGCTGCGAGAATTCCTTGAACCTTCACATAGATG 6879
Db 6780 CGGCTGCTCTCCACGGATCGAGAATGCTGCGAGGATTCCTTGAACCGCACATTTAGT 6839
QY 6880 TCATCATGGAAGATTGCACTACACCTCTCTTTTGTGGAGTAGCCGAGAGATGCGCTGTGT 6939
Db 6840 CCATCATGGAGACTGCAGTACACCTCTCTTTTGTGGTAGTAGCCGAGAGATGCGCTGTAT 6899
QY 6940 GGGGAGAAGACATACCCGCACCTCCATCGCAGACTTATCTCGGTTACTGAGACAGCC 6999
Db 6900 GGGGAGAAGACATCCCCGCTACTCCATCGCCAGCACTTATCTCGGTTACTGAGACAGCT 6959
QY 7000 CAGATTGAAGACCCCGTCGGTGTCTCTCTCGCAGAGATACCCGCTCTGACTCAT 7059
Db 6960 CAGATTGAAGACCCCGTCGGTGTCTCTCTCGCAGAGATACCCGCTCTGACTCAT 7019
QY 7060 TCGAGGTCTATCCAGAGTCCGAGACAGCCGAAGGGGAGGAAGCGTCTCAACGTGGCTC 7119
Db 7020 TCGAGGTCTATCCAGAGTCCGAGACAGCCGAAGGGGAGGAAGCGTCTCAACGTGGCTC 7079
QY 7120 TTTCCGTACTAAAGCCCTGTTTTCACAGAGCGGATGCCACAAGAAGCTTACCGTTAAGA 7179
Db 7080 TTTCCGTATTAGAAGCCCTATTTCACAGAGCGGACGCCAGCAAGGCTTACCGTCAAGA 7139
QY 7180 TGCTATGCTGTTCAGAGAGCGCTAACACGCTTCTTTCATTTGGATTGAGGTCGCTG 7239
Db 7140 TGCTGTGCTGCTTGAAGAAGCGTCACGCGCTTTTCTCATTTGGGTTGAGCGTGGTG 7199
QY 7240 AGTGCGCAAGCCTGTGTGAGATTGGAATCCAGAACCATACAGCCATTATGTGACAAAGTGC 7299
Db 7200 ATGTTGCTAGCCTGTGTGAGATTGGAATCCAGAACCATACAGCCATTATGTGACAAAGTGC 7259
QY 7300 GCATCCCGTTGAATTGACGTTGGGTGCTTGGTGGCAATGAACCTTACCTTTGAATGTG 7359
Db 7260 GCATCCCGTTGAATTGACGTTGGGTGCTTGGTGGCAATGAACCTTACCTTTGAATGTG 7319
QY 7360 ACAAGTGTGAGCTAGGCAAGAGACCTTGGCTTCTCTTACATTTGGTCTGGGGTGC 7419
Db 7320 ACNAGTGTGAGCTAGGCAAGAAACCTTGGGCTCCTTCTCTTACATTTGGTCTGGAGTGC 7379
QY 7420 CACTGACGAGGGCCACTCCGGCCAAAGCCCTGTGGTGAAGCCGTTGGCTCCTTTGCTGG 7479
Db 7380 CGCTGACTAGGGCCACCGCGCCAAAGCCTCCGTTGGTGAAGCCGTTGGCTCTTTATTAG 7439
QY 7480 TGGCCGACACCACCAAGGTGTATGTACCAACCCGGACAATGTTGGGAGAAGATTGACA 7539
Db 7440 TGGCCGACACTACTAAGTGTATGTATACCAATCCAGACAATGTGGGACGAGGTTGGACA 7499
QY 7540 AGGTTACCTTCTGGCGTCCCTAGGTTTCATGACAAATTCCTCTGTCGACCTCCATAGAGC 7599
Db 7500 AGGTGACCTTCTGGCGTCTCTAGGTTTCATGATTAAGTACCTCTGACTCTATTGAGC 7559
QY 7600 GGGCTTAAGGGCAGCTCAAGCCTGCCTTAAGCATGGGTTACACTTATGAGGAGCAATAA 7659
Db 7560 GGGCTTAAGGGCCGCTCAAGCCTGCCTTAAGCATGGGTTACACTTATGAGGAGCAATAA 7619
QY 7660 GGACTGTAAAGGCCACATGCTGCCATTGGGTGGGGATCTAAGGTGTGCGTCAAGGACCTCG 7719
Db 7620 GGACTGTAAAGGCCACATGCTGCCATTGGGTGGGGATCTAAGGTGTGCGTTAAGGACTTAG 7679
QY 7720 CCACCCCTGCGGGGAAGATGGCTGTCCATGACCCGCTCCAGAGATACTTGAAGGAGCGC 7779
Db 7680 CCACCCCTGCGGGGAAGATGGCCGTCCTATGACCCGCTCCAGAGATACTTGAAGGAGCTC 7739

QY 7780 CAGTCCCTTTACTCTTACTGTGAAAAAGAAAGTGTCTTCAAAGACCCGAAAGAGAGA 7839
Db 7740 CGTCCCTCTTACTCTTACTGTGAAAAAGAGAGTGTCTTCAAAGACCCGAAAGAGGAGG 7799
QY 7840 AGGCCCCCGGCTCAATGTTGTTCCTCCCTCGACTTCGGGATAGCTGAAAAGCTTTATTC 7899
Db 7800 AGGCCCCCGGCTCAATGTTGTTCCTCCCTCGACTTCGGGATAGCTGAAAAGCTCATCT 7859
QY 7900 TGGGAGACCTTCGACGGGTAGCAAGCGGTGTGGGGGGGCGCTACGCTTCCAGTACA 7959
Db 7860 TGGGAGACCCAGACCGGGTAGCCAAAGCGGTGTGGGGGGGCGCTACGCTTCCAGTACA 7919
QY 7960 CCCCAAATCAGGAAATTAGGAGATGCTCAAAGTGTGGGAATCAAAGAGACACCATTCG 8019
Db 7920 CCCCAAATCAGGAGTTAAGGAGATGCTCAAAGTATGGGAGTCTAAGAAGACCCCTTGG 7979
QY 8020 CCATCTGTGGACGCCACATGCTTCGACAGTAGGATTAAGTAAAGAGAGCTGGCGTGG 8079
Db 7980 CCATCTGTGGACGCCACCTGCTTCGACAGTAGGATTAAGTAAAGAGAGCTGGCGTGG 8039
QY 8080 AGACAGAGCTTTATGCCCTTGGCTTCAGACCATCCAGAATGGGTGGCTGCCCTGGGAAAT 8139
Db 8040 AGACAGAGCTGTACGCTCTGGGCTCTGACCATCCAGAATGGGTGGCGCACTTGGGAAAT 8099
QY 8140 ACTATGCTCTTGGCAAAATGGTAAACCCCGAGGGGTGCCAGTGGGTGAGAGGTATTGTA 8199
Db 8100 ACTATGCTCTAGGCAACCATGGTCAACCCGGAAGGGTGGCGCTCGTGAGAGGTATTGCA 8159
QY 8200 GATCTCAGGGTCTTTGACACCACTGCGAGCAACTGCTTGTGACTTGTATATCAAGGTGA 8259
Db 8160 GATCTCAGGGTCTTAACTAGCGGAGCAACTGCTTGTGACTTGTATATCAAGGTGA 8219
QY 8260 RAGCCGCTGTGAGAGGTGGGGCTGAAAAATGCTCCGCTCCATCCGTCGCGATGACT 8319
Db 8220 RAGCCGCTGTGAGAGGTGGGGCTGAAAAATGCTCTCTCTCATAGCGCGGATGACT 8279
QY 8320 GTTGTATCATATGCAAGCGGCTGTGTGATCTTGGACACGCTTTGGCAGAGCCCTGG 8379
Db 8280 GCTTGTATCATATGTCAGCGGCGGCTGCGACCCCAAGCGAGCTTTGGCAGAGCCCTAG 8339
QY 8380 CGAGTACGGGTACGATGCGAGCCTTCGTATCATGCACTGACAGAGCGCCCTCTCT 8439
Db 8340 CGAGTATGGGTACGCTGCGAGCCTCATATCATGCACTTGGACAGCGCCCTCTCT 8399
QY 8440 GCTCCACTTGGCTAGCTGAGTGCATGAGATGGGAAGCGCAATTTCTCTGACACAGG 8499
Db 8400 GCTCCACTTGGCTTGTGAGTGCATGAGATGGGAAGCGCAATTTCTCTGACACAGG 8459
QY 8500 ACTTTTCGAGGGCCCTCGCTCGCATGTGAGCGAGTACAGTGACCAATGGCTTCGGCCA 8559
Db 8460 ACTTCGGAGGCGGCTCGCTCGCATGTGAGTGCATGATAGTACCCGATGGCTTCGGCA 8519
QY 8560 TCGGTTACATCTCTATACCTTGGCATCTTATCACAGGTGGGTGCTATCATCTCCTCAG 8619
Db 8520 TCGGTTACATCTCTCTTATCTTGGCACCCCATCACAGGTGGGTGCTATCATCTCCTCAG 8579
QY 8620 TGCTCACCTGCGGTTTAGGGTGGTGCACACCGCTCTGATCTCTGTTGTCGAGGTAC 8679
Db 8580 TGCTAACGTGGCATTTAGGGGTGGGACACCGCTCTGATCCCGGTTGGTCCAGGTAC 8639
QY 8680 ATGTTAAATTACTTACAAGTTTCCACTGGCAAACTGCCTAACATCATCTGGGCGCTCCAG 8739
Db 8640 ATGGTAACTACTACAAGTTTCCACTGGCAAACTGCCTAACATCATCTGGGCGCTCCAG 8699
QY 8740 GACACGAGCGTTGAGGTTACCGCAGACACAACCTAAGACAAAAATGGAGGTGGCAAGG 8799
Db 8700 GACACGAGCGTTGAGGTTACCGCAGACACAACCTAAGACAAAAATGGAGGTGGTAAAG 8759
QY 8800 TGCTGAGCGACTCAAGCTCCCTGGCTTAGCAGTCCACCGGAAGAGCCCGGGCATTCG 8859
Db 8760 TTCTGAGCGACTCAAGCTCCCTGGCTTAGCAGTCCACCGGAAGAGCCCGGGCGTTCG 8819

QY 8860 GAACGGGTATGCTCCCGTCCGCGGTTGGGCTGAGTTGGCTAGGGGCTGTGTTGGCGTC 8919
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 8820 GAACACGATGCTCCGCTCGCGGTTGGGCTGAGTTGGCTAGGGCTGTGTTGGCATC 8879
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 8920 CAGGCTGCGGCTTCCCGTCCGCGATGCTGGTATCCCGGGGGTGTCCCGCTTCC 8979
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 8880 CAGGCTACGCTTCCCGCTGAGATTGCTGGTATCCCGGGGGTGTCCCGCTCTCC 8939
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 8980 CCCCCTATATGGGGTGGTTCATCAATTGGATTTCACAGCCAGAGAGTCGCTGGCGGT 9039
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 8940 CCCCCTATATGGGGTGGTTCACCAATTGGATTTCACAGCCAGAGAGTCGCTGGCGGT 8999
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 9040 GGTGGGGTCTTAGCGCTGCTCATGCTAGCCCTCTTCGGGTGAACCTAAATTCATCTGT 9099
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 9000 GGTGGGGTCTTAGCGCTGCTCATGCTAGCCCTCTTCGGGTGAACCTAAATTCATCTGT 9059
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 9100 GCGGCAAGTCCGCTGACTGATCATCTGAGGAGGTTCCCGCCCTCCCGCCCGCAGGG 9159
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 9060 GCGGCAAGTCCGCTGACTGATCATCTGAGGAGGTTCCCGCCCTCCCGCCCGCAGGG 9119
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 9160 GTCTCCCGCTGGGTAAAGGCGCGGCTTGGGAGGATGTTACTAAACCCCGCTG 9219
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 9120 GTCTCCCGCTGGGTAAAGGCGCGGCTTGGGAGGATGTTACTAAACCCCGCTG 9179
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 9220 GCAGGGTCAAGCCTGATGTGCTAATGCACTGCCACTTCGTTGGCGGGTCGCTACCTTA 9279
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 9180 GCAGGGTAAAGCCTGATGTGCTAATGCACTGCCACTTCGTTGGCGGGTCGCTACCTTA 9239
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 9280 TAGGTTAATCCGCTGACTACGGGCTGCTCGCAGAGCCCTCCCGGATGGGCGACAGTGCAC 9339
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 9240 TAGGTTAATCCGCTGACTACGGGCTGCTCGCAGAGCCCTCCCGGATGGGCGACAGTGCAC 9299
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 9340 TGTGATCTGAAGGGGTGCACCCCGGTA 9367
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 9300 TGAGATCTGAAGGGTGCACCCCGGTA 9327
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
RESULT 11
AAV56242
ID AAV56242 standard; cdna; 9327 BP.
XX
AC AAV56242;
XX
DT 06-NOV-1998 (first entry)
XX
DE HGV isolate 32HGV-6 cdna from PNF2161.
XX
KW Immunoreactive; detection; antibody; alanine aminotransferase;
KW Non-A, Non-B, Non-C, Non-D, Non-E hepatitis virus; ds.
XX
OS Hepatitis G virus.
XX
PN US5766840-A.
XX
PD 16-JUN-1998.
XX
PF 05-JUN-1995; 95US-0466033.
XX
PR 19-MAY-1995; 95US-0444733.
PR 20-MAY-1994; 94US-0246985.
PR 03-AUG-1994; 94US-0285543.
PR 03-AUG-1994; 94US-0285558.
PR 03-AUG-1994; 94US-0285561.
PR 26-OCT-1994; 94US-0329729.
PR 23-NOV-1994; 94US-0344271.
PR 16-DEC-1994; 94US-0357509.
PR 15-FEB-1995; 95US-0389886.
PR 05-JUN-1995; 95US-0466033.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fry KE, Kim JP, Linnen JM, Wages J, Young LM;
XX

DR WPI; 1998-361677/31.
XX
PT Antibody to hepatitis G virus protein - useful for diagnosis of
PT hepatitis G virus infection
PS
XX Example 18; Column 337-346; 204pp; English.
CC This sequence is a used in a method which detects Non-A, Non-B, Non-C,
CC Non-D, Non-E hepatitis G virus (HGV) in a biological fluid sample, e.g.
CC from a test subject, especially using a kit comprising an anti-HGV
CC antibody preparation and a reporter for detecting binding of an HGV
CC polypeptide antigen to the antibody, preferably where the antibody is
CC monoclonal and/or is attached to a solid support and where the reporter
CC is a labelled monoclonal antibody or a labelled competing antigen. The
CC HGV is characterised by producing elevated serum alanine aminotransferase
CC levels in an infected primate, being serologically distinct from
CC hepatitis A, B, C, D and E viruses and having a viral genome containing a
CC nucleic acid region that is selectively hybridisable with a polypeptide
CC having 203 base pairs as given in the specification.
XX
SQ Sequence 9327 BP; 1682 A; 2532 C; 2984 G; 2129 T; 0 other;
Query Match 83.9%; Score 7885.6; DB 19; Length 9327;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 8433; Conservative 0; Mismatches 894; Indels 1; Gaps 1;
QY 40 GCAGGCCCATAAACCGAGCGCTTATCTAAGTAGACGCAATGACTCGCGCGACTCGCG 99
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 1 GCAAGCCCCAGAAACCGAGCGCTTATCTAAGTAGACGCAATGACTCGCGCGACTCGCG 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 100 ACCGGCCAAAAGTGGTGGATGGGTGGTGACAGGGTTGGTAGTCTGAATCCCGTCTAT 159
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 61 ACCGGCCAAAAGTGGTGGATGGGTGGTGACAGGGTTGGTAGTCTGAATCCCGTCTAC 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 160 CTTGGTAGCCACTATAGTGGGTCTTAAAGAGAAGGTCAAGACTCTCTTGTGCTCGGCG 219
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 121 CTTGGTAGCCACTATAGTGGGTCTTAAAGAGAAGGTTAAGATTCTTGTGCTCGGCG 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 220 GAGACCGCGCAGGTCCACAGGTGCTGGCCCTACCGGTGTAATAAGGGCCCGACGTCTAG 279
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 181 GAGACCGCGCAGGTCCACAGGTGTTGGCCCTACCGGTGGGAATAAGGGCCCGACGTCTAG 240
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 280 GCTCGCTGTTAAACCGAGCCGCTACCCACCTGGGCAAGAGCGCCACCTAGCGTCCAC 339
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 241 GCTCGCTGTTAAACCGAGCCGCTTACCCACCTGGGCAAGAGCGCCACCTAGCGTCCAC 300
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 340 GTCCGCTTCAATGCTCTCTTGACCAATAGTCTTATCCCGCGAGTTGACAAGGACCACT 399
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 301 GTCCGCTTCAATGCTCTCTTGACCAATAGGCTAGCCGCGAGTTGACAAGGACCACT 360
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 400 GGGGGCGGGGGTATGGGAAGGACCCCAACCCCTGCCCCCTCCCGGTGGCGGGGAAAT 459
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 361 GGGGGCGGGGGCT-TGGAGAGGGACTCCAAGTCCCGCCCTCCCGGTGGCGGGGAAAT 419
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 460 GCATGGGGCCACCCAGCTCCGCGGGGCGCTGCAGCGGGGTAGCCCCAAGAACTCTTCGGG 519
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 420 GCATGGGGCCACCCAGCTCCGCGGGGCGCTGCAGCGGGGTAGCCCCAAGAACTCTTCGGG 479
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 520 TGAGGGCGGGTGGCATTTCTTTTATACCATATGCGAGTCTCTCTCTCTCTCTCG 579
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QY 580 TGGTTGAGGGCGGGGCAATTTCTGGCCCCCGCCACCCACGCTTGTGAGAGCAATGGGCAAT 639
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 540 TGGTTGAGGGCGGGGCAATTTCTGGCCCCCGCCACCCACGCTTGTGAGAGCAATGGGCAAT 599
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 640 ATTTCTCACAATTTGCTGTGCCCCCGGAAGACATCGGGTTCTGCTGGAAGGGGATGCC 699
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Db 600 ATTTCTCACAATTTGCTGTGCCCCCGGAAGACATCGGGTTCTGCTGGAAGGGGATGCC 659
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
QY 700 TGGTGGCCCTGGGGTGCACGGTTTGCACCGACGCTTCTGCGCCACTGTATCAGGCGGGTT 759
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
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QY 760 TGGCTGTGCGGCTGGCAAGTCCGCGGCCAGCTCGTTGGGAACCTGGGAGCGCTGTACG 819
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QY 820 GGGCCCTGTCGGCTCGGCTTACGTAGCGGGATCCTGGGTCTGGCGAGGTTACTCGG 879
DB 780 GGGCCCTGTCGGCTCGGCTTATGGCTGGATCCTGGGCTGGGTGAGGTGTACTCGG 839
QY 880 GGGTCTGTACAGTTGGTGTGGTTCGAGCGCGGCTCTACCTGTAGTCCCAACCTCAACT 939
DB 840 GTGTCTTACAGTGGGAGTCCGGTTGACCGCGCGGATCTACCGGTGCCCTAACCTGACGT 899
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DB 900 GTGCACTCGCGTGTGAGTTAAAGTGGAAAGTGAAGTTTGGAGATGACTGAACACTGG 959
QY 1000 CTTCCAATTTACTGGATTTGGAAATACCTTTGGAAAGTCCCAATTTGAAATTTGGAGAGAG 1059
DB 960 CTTCCAATTTACTGGATTTCTGGAATACCTCTGGAAGTCCCAATTTGATTTCTGGAGAGCG 1019
QY 1060 TGAATGAGCTGACCCCTCTGTTGGTGTGGTGGCGCCCATTTGCTTGGTGGACACGGA 1119
DB 1020 TGAATGAGCTGACCCCTCTGTTGGTGTGGTGGCGCCCATTTGCTTGGTGGACACGGA 1079
QY 1120 TTGTCATGTGTTTCCCTGCTGGTGACGATGGCGGGGATGTTGAAAGCGCCCGCCCTCGG 1179
DB 1080 TTGTCATGTGTTTCCCTGCTGGTGACGATGGCGGGGATGTTGAAAGCGCCCGCCCTCGG 1139
QY 1180 TTTTGGGGTCCGCGCCCTTTGACTACGGGTTGAAGTGGCAGTATGCTCCTCGAGGGCTA 1239
DB 1140 TTTTGGGGTCCGCGCCCTTTGACTACGGGTTGACTTTGGCAGACCTGCTCTTGGAGGGCA 1199
QY 1240 ACGGGTCCGCTATCCCACTGGGAGAGGTTGGGATCGAGGGATGTACGCTCTTGT 1299
DB 1200 ACGGTTCCGCTTTTTCGACTGGGAGAGGTTGGGACCGTGGGAACGTTACGCTTCACT 1259
QY 1300 GTGACTGCCGCCAACGCGCCCTGGGTTGGGTCGCGGCTTTTGGCAAGCGGTTGGTGCG 1359
DB 1260 GTGACTGCCCTTAAAGCGCCCTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1319
QY 1360 GGGACCCCATACCCATNTGGAGCAGCGGACAAACAGTGGGCGCTTATCATGCCGCCAAT 1419
DB 1320 GTGACCCCATACCTTATTTGGAGCCAGCGGCAAAATCAGTGGGCGCTTTCATGCCGCCA 1379
QY 1420 ATGTCTATGSGTGTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1479
DB 1380 ATGTCTATGSGTGTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1439
QY 1480 CCGGCGGTGCTGATTCGAAGATCGATGTGGAGTTTGGTGGCGGTTGGATCTGCCAGCT 1539
DB 1440 CCAGTGTGCGGACTCGAAGATAGATGTGGAGTTTGTGGCAGTTGGCTCTGCCACCT 1499
QY 1540 GCACATAGCCGCTTAGGGTCAATCGGATCGGACACAGGTGGTGTAGCTCTCCGAGTGG 1599
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QY 1600 GAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1659
DB 1560 GAATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1619
QY 1660 GGGACTGCTGGCGGCAACCGGCTGGGTTAGATTTCCCTTTCCATCGGTGGCGACCGGGC 1719
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QY 1720 CTCGGCTGACAAAGACTTGGAGCTGTGCCCTTGTCTGCTGCTGCTGCTGCTGCTGCTG 1779
DB 1680 CTCGGCTGACAAAGACTTGGAGCTGTGCCCTTGTCTGCTGCTGCTGCTGCTGCTGCTG 1739
QY 1780 TAAGGGGCCCTGGGCAACCGGAGAGGCAACCGGCTGGGCTGGGCTGGGCTGGGCTGGG 1839
DB 1740 TTAGGGGGCCCTGGGCAACCGGAGGCAACCGGCTGGGCTGGGCTGGGCTGGGCTGGG 1799

QY 1840 GGTCTCTACCATGATGACCAAGATCCCGGATTCCTTCGATTTGGTGAATGTCCACACCA 1899
DB 1800 GGTCTCTACCATGATGACCAAGATCCCGGATTCCTTCGATTTGGTGAATGTCCACACCA 1859
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DB 1860 CCATAGAGCCTCGGACTCGAAGTTCCTCCCGGAGTCCCGCCCATTAACAAC 1919
QY 1960 GATAGCGCTAGGACCGAAGTGTCTGAGGCATTTGGCGGAGCTGGCTTACGGGGGGT 2019
DB 1920 GATAGCGCTAGGACCGAAGTGTCTGAGGCATTTGGCGGAGCTGGCTTACGGGGGGT 1979
QY 2020 TCTAGAGCCTCTGGTTCGAGGTTCGAGGTGATGGAGCGCCGAAATCCGGTTTGC 2079
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DB 2040 CGGGTTCGATGGCTGCTCTGAGTACCTGACGGGTTCATACAGCTTCAGGGGCA 2099
QY 2140 TGCAGAGGTGATCGGCGCAACTTCATCCCTCCAGCTGGTTCCTTGGATTTG 2199
DB 2100 TGCAGAGGTGATCGGCGCAACTTCATCCCTCCAGCTGGTTCCTTGGATTTG 2159
QY 2200 TATTTGCTCTCTATCTGATGAAGCTGGCTGAGCAGCTGGTTCCTGCTTGCCTTGC 2259
DB 2160 TATTTGCTCTCTATCTGATGAAGCTGGCTGAGCAGCTGGTTCCTGCTTGCCTTGC 2219
QY 2260 TTTCTGCTGTGGTGGGTGAACAGTTGGCGTTCATAGACTGCGGCTGTGGAGCTG 2319
DB 2220 TGTCTGATGTTGGTGGGTGAACAGTTGGCGTTCATAGACTGCGGCTGTGGAGCTG 2279
QY 2320 CGGTGGCGGTGATGTTTGGCGGCTTCCTGCTGATGCTGCTTGGCTTCCACCTG 2379
DB 2280 CGGTGGCGGTGATGTTTGGCGGCTTCCTGCTGATGCTGCTTGGCTTCCACCTG 2339
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DB 2400 GCTCATGTTCTGCTGTTGTGGAAGCTGCTGCGGAGCTTTCCGCTGGCCTTCTGA 2459
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QY 2560 TCACATTCGAGTGGACACTTCGGTTCGGCTGGGCTGGGCTGGGCTGGGCTGGG 2619
DB 2520 TCACATTCGAGTGGACACTTCGGTTCGGCTGGGCTGGGCTGGGCTGGGCTGGG 2579
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DB 2580 CCATAGCGCTCTGAGCTCAATGAGCGGAGGGGTGGAGACAAAGCGCTGATCTATA 2639
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DB 2640 GAGCTGTGTAAAGGTTACAGGCTGTCGCCAGAGGTGTGGCGAGCCCTCGGG 2699
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DB 2700 AGGGCGCTCTACCAAGCTTCGACCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2759
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DB 2760 ATGCTGTGATGATGTTGGTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 2819
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DB 2820 ATGGCCCTGGAGGAGATCTTGGTTCGCCGCTTCGCTTGGCTTGGCTTGGCTTGG 2879
QY 2920 TTTAGTGTGTGATGGCGGGGAGAGGCCACCACTCCGACTGGTCTCCAAGATGT 2979

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QY 5200 CAGACTGGGATGTAAGGGGGTGGCAGCCCCCTTTATCGGCATGGAGACCGCACGC 5259
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QY 5380 TCATGACCCTGTCGATCGGGGAGTGTCTGCTTGGCCAGGCTAAGACGGCCGAGGCT 5439
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DB 5400 ACACAGCACCAAGTGGCTGCTGCTATACGGGGACGGGGCCGTTCGCCACTG 5459
QY 5500 TTTCAATTGTTGACAAAGCTCTTTCGGCGGGGCTGGCGGCGGTGGTAGGCCATTGCCACA 5559
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QY 5560 GTGTAAATAGCTCGGGAGTGGGCGCTATGGGCGTCTTAGAGCCCTCCATTGGCTGCTG 5619
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QY 5620 CCGCTTCCCTACCTATGGGGTGGGCTCGGAGGCAACGGCGCAACCCCTTAGCCTCCG 5679
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QY 5860 GGAACTATCATCAGAAGATCTGTGGTATGCCATCCAGTGTCTAACCGTCCGGGGGAG 5919
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QY 5920 GACTTGGGGGATCGCCCTCGGGTGGTGTGTACTCAGCTAACAACTCTGGCATTACCA 5979
DB 5880 GCGTTCGGGGATCGCTCTCGGTTGGTTTGTATTTCAGCTAACAACTCTGGCATTACCA 5939
QY 5980 CTTGGTTGAACCGCTCTGCTACTACATTCGCAAGTTCCTCATGCTACCTCGAGCTTACT 6039
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QY 6040 TTCAGAGCCGATCTGTGACAAGGCTCTAGCTGTGCTCGGAGCTTTGAGCCCTCACATC 6099
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QY 6100 GCACCGTGTTCCTCGTTCACAGGAGCCCTAAGGTGATGAGGTTAGAGTGGGTAGC 6159
DB 6060 GCACAGTGTTCCTCGTTCACAGGAGCCCTAAGGTGATGAGGTACAGGTGGGTATG 6119
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DB 6120 TCTGGGACTTGGGAGTGCATCGCTCAAGTGGGCTAGTGGCCAGCTTCGGG 6179

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QY 6400 TGGGAGACGTCCTGTGAACTGCTGGGCTATGGCGAGACGTCGCTTTCGCTCGCCTCAG 6459
DB 6360 TGGGAGACTCTCCTGTGAACATGCTGGGTACGGTGAACGTCGCTCTCTCTGGCCTCCG 6419
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DB 6420 ACACCCCGAAGTGTGTGCTTTCGGGACGCTCTGGGTGGGCTGAGGTGGTGGTACCCCTA 6479
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QY 6580 CTGCTGTTGCTGAGCGCTATTACGTCGACGGCATACCGGCTCTCATGGAGCGGAGCGCG 6639
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QY 6640 GAGCGCTGCCATGCTATGCGCCCTGGGCAAGTGTACCATTTGACGGGGAACGCTACA 6699
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QY 7300 GCACCTCCGCTTGAATTGACAGTTGGTGTGCTTGTGGGCAATGAACCTTACCTTTGAATGTG 7359

Db	7260	GCATCCGCTTGAATTTGCAGGTTGGGTGCTTGGTGGCAATGAATACCTTTGAATGTG	7319
Qy	7360	ACAAGTGTAGGCTAGCGAAGACACTTGGCTTCCTCTCTTACATTTGGTCTGGGTGC	7419
Db	7320	ACAAGTGTAGGCTAGCAAGAACTTGGCCCTCCTCTCTTACATTTGGTCTGGAGTC	7379
Qy	7420	CACTGACGAGGGCACTCCGGCCAAAGCCCTGTGGTGAGCCGGTTGGCTCTTGCTGG	7479
Db	7380	CGCTGACTAGGGCCACCGCGCCAGGCTCCCGTGTGAGCGCGTTGGCTCTTTATTAG	7439
Qy	7480	TGGCCGACACCCAAAGTGTATGTACCAACCCGGACAATGTTGGGAGAAGAGTTGACA	7539
Db	7440	TGGCCGACACTACTAAGGTGTATGTACCAATCCAGACAATCTGGACGGAGGTGACA	7499
Qy	7540	AGGTTACTTCTCGCTGCCCTAGGGTTCATGACAAATTCCTCGTGGACTCCATAGAC	7599
Db	7500	AGGTGACCTTCTGGCTGTCTCTAGGGTTCATGATTAAGTACCTCGTGGACTCTATTGAGC	7559
Qy	7600	CGCTTAAGAGGCGAGCTCAAGCTGCGCTAAGCATGGGTTACACTTATGAGGAGGCAATAA	7659
Db	7560	CGCTAAGAGGGCGCTCAAGCTGCGCTAAGCATGGGTTACACTTATGAGGAGCAATAA	7619
Qy	7660	GGACTGTAAGGCCACATGCTGCCATGGCTGGGATCTAAGGTCTCGTCAAGGACCTCG	7719
Db	7620	GGACTGTAAGGCCACATGCTGCCATGGCTGGGATCTAAGGTCTCGTTAAGGACTTAG	7679
Qy	7720	CCACCCCTGGGGGAAGATGGCTGTCCATGACCGGCTCCAGGACATACTTGAAGGGACGC	7779
Db	7680	CCACCCCGGGGAAGATGGCGTCCATGACCGCTCCAGGAGATACTTGAAGGGACTC	7739
Qy	7780	CAGTCCCTTTACTCTTACTGTGAAAGAGAGTCTTCTCAAGACCGGAAAGGAAGAGA	7839
Db	7740	CGTCCCTTTACTCTTACTGTGAAAGAGAGTGTCTTCAAGACCGGAGAGGAGG	7799
Qy	7840	AGGCCCCCGCCCTCATTTGTTCCCCCCCCCTGGACTCCGGTAGCTGAAAAGCTTATTC	7899
Db	7800	AGGCCCCCGCCCTCATTTGTTCCCCCCCCCTGGACTCCGGTAGCTGAAAAGCTATCT	7859
Qy	7900	TGGGAGACCTTGACGGGTAGCCAGAGGGGTGTTGGGGGGGGCCTAGCCCTCCAGTACA	7959
Db	7860	TGGGAGACCCAGACGGGTAGCCAGAGGGGTGTTGGGGGGGGCCTAGCCCTCCAGTACA	7919
Qy	7960	CCCCAAATACGCAATTAGGGAGATGCTCAAACTGTGGGAATCAAGAAGACACCATGCG	8019
Db	7920	CCCCAAATACGCAATTAAGGAGATGCTCAAGCTATGGGAGTCTTAAGAGACCCCTTGGC	7979
Qy	8020	CCATCTGTGGAGCCACATGCTTCGACAGTAGCATAACTGAAGAGGACGTGGCGCTGG	8079
Db	7980	CCATCTGTGGAGCCACCTGCTTCGACAGTAGCATAACTGAAGAGGACGTGGCTTTGG	8039
Qy	8080	AGACAGAGCTTTATGCCCTGGCTTCAGACCATCCAGATGGGTGCTGTCCTGGGGAAT	8139
Db	8040	AGACAGAGCTGTAGCTCTGGCTCTGACATCCAGAAATGGGTGCGGCGCACTTGGGAAT	8099
Qy	8140	ACTATGCTCTGCGACAATGTAAACCCCGAGGGGTGCCAGTGGGTGAGAGTATTGTA	8199
Db	8100	ACTATGCTCTGAGCCACATTTGGTACCCCGAAGGGGTGCCGTGCGTGAAGAGTATTGCA	8159
Qy	8200	GATCCTCAGGGGTCTTGACACACAGTGGGAGCACTGCTTGACTTGTCTATATCAAGGTGA	8259
Db	8160	GATCCTCGGTGTCTTAACAATAGCGCGAGCACTGCTTGACCTGCTACATCAAGGTGA	8219
Qy	8260	AAGCGGCTGTGAGAGGTTGGGCTGAATAATGTCTCGCTCCTCATCGCTGGGAGTGA	8319
Db	8220	AAGCGGCTGTGAGAGGTTGGGCTGAATAATGTCTCTCTCTCATAGCGGGCATGACT	8279
Qy	8320	GTTTGATCATATCGAAGCGCTGTGTGCGATCCCTPAGCGAGCTTTGGGAGAGCCCTGG	8379
Db	8280	GCTTGATCATATGTAGCGGCCAGTGTGGACCCGAAGCGCTTTGGGAGAGCCCTAG	8339
Qy	8380	CGAGCTACGGGTACGATGCGAGCCCTTGTATATGCATCACTGGACACGCGCCCTTCT	8439

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RESULT 12
AAX16505
ID AAX1
XX
AC AAX1
XX
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AAX16505 standard; cDNA; 9327 BP.

AA
AC
AAAX16505;

XX

RESULT 12
AA16505
ID AA16505 standard; cDNA; 9327 BP.
XX
AC
AA16505;
XX

AAX16505 standard; cDNA; 9327 BP.

AA
AC
AAAX16505;

XX

22-JUL-1999 (first entry)
Polynucleotide sequence of HGV clone 32-HGV94-6.
Hepatitis G virus; HGV; HCV-E2 antigen; vaccine; viral replication;
treatment; HGV infection; antisense; ds.
Hepatitis G virus.
US5874563-A.
23-FEB-1999.
05-JUN-1995; 95US-0485910.
19-MAY-1995; 95US-0444733.
PR 20-MAY-1994; 94US-0246985.
PR 03-AUG-1994; 94US-0285543.
PR 03-AUG-1994; 94US-0285558.
PR 26-OCT-1994; 94US-0329729.
PR 23-NOV-1994; 94US-0344271.
PR 16-DEC-1994; 94US-0357509.
PR 15-FEB-1995; 95US-0389886.
PR 05-JUN-1995; 95US-0485910.
(GENE-) GENELABS TECHNOLOGIES INC.
Fry KE, Kim JP, Linnen JM, Wages J, Young LM;
WPI; 1999-180067/15.
Isolated polynucleotide sequences derived from the Hepatitis G Virus
that encode the E2 antigen - useful for producing vaccines and
inhibitors against Hepatitis G, and for assays to detect the virus
in a sample
Example 18; Column 337-344; 206pp; English.
The specification describes isolated polynucleotide sequences, derived
from a Non-A, Non-B, Non-C, Non-D, Non-E (N-(ABCD)E) Hepatitis Virus
(designated Hepatitis G or HGV). HGV is characterised by stimulating
production of serum alanine aminotransferase in primates infected with
the virus, being serologically distinct from the Hepatitis A, B, C, D
and E viruses, and being a member of the Flaviviridae virus family.
The HGV-E2 antigens, encoded by the polynucleotide sequences of the
invention, may be produced by standard recombinant DNA techniques,
and used in the preparation of vaccines. Anti-sense oligonucleotides
and oligonucleotide analogues which encode portions of the sequences
disclosed in the specification may be used to prevent expression of
the HGV-E2 genes by blocking transcription and preventing them
functioning normally in viral replication. Antisense sequences may be
used in this way as part of a treatment strategy against HGV infection.
The single stranded nature of the viral genome makes HGV highly
susceptible to inhibition in this way. The present sequence represents
the polynucleotide sequence of HGV clone 32-HGV94-6.

Query Match 83.9%; Score 7885.6; DB 20; Length 9327;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 8433; Conservative 0; Mismatches 894; Indels 1; Gaps 1;

QY 40 GCAAGCCCCATAACCGACGCTATCTAAGTAGACGAATGACTCGGCCGGCAGCTCGCGG 99
DB 1 GCAAGCCCCAGAACCAGCGCTTATCTAAGTAGACGAATGACTCGGCCGGCAGCTCGCGG 60

QY 100 ACCGGCCAAAAAGGTGGTGAGTGGGTGGTGACAGGGTTGGTAGGTGCTAAATCCCGGTCAT 159
DB 61 ACCGGCCAAAAGGTGGTGAGTGGGTGGTGACAGGGTTGGTAGGTGCTAAATCCCGGTAC 120

QY 160 CCTGGTAGCCACTATAGGTGGGTCTTAAGAGAAGGTCAAGACTCCTCTTGTGCCTCGCGC 219
DB 121 CTTCGGTAGCCACTATAGGTGGGTCTTAAGAGAAGGTCAAGACTCCTCTTGTGCCTCGCGC 180

QY 1300 GTGACTGCCCAAGGCCCTGGGTTTGGGTCCCGGCTTTTGGCAGCGGTGGTGGG 1359
DB 1260 GTGACTGCCCTAACGGCCCTGGGTGGTGGCAGCCTTTGGCAAGCAATCGCTGGG 1319
QY 1360 GCGACCCCATCACCCATGAGACCAAGCAAAAACAGTAGTGGCCCTATCATGCCCCCAAT 1419
DB 1320 GTGACCCCATCACATTATTGGAGCCACGGGCAAAATAGTGGCCCTTTTCATGGCCCCAGT 1379
QY 1420 ATGTCATGGGTCTGTGTCCTAAGTCGCTGTGGGTCCGCTCTCTGTGTTGCCCTCGA 1479
DB 1380 ATGTCATGGGTCTGTACAGTCACTTGCCTGTGGGTTCGCTCTTGGTATGCCCTCCA 1439
QY 1480 CCGCGGTCTGTGATTGAAGATCATGTGTGGATTGGTGCCGGTTGGATCTGCCAGCT 1539
DB 1440 CCAGTGTGCGGACTCGAAGATAGATGTGGAGTTTGTAGTGCCAGTTGGCTCTGCCACCT 1499
QY 1540 GCACCATAGCCGCTTAGGGTTCATCGATCGCGACAGGTGGTGTAGCTCTCCAGTGGG 1599
DB 1500 GCACCATAGCCGCACTTGGATCATCGATCGCGACAGGTGCCGTGGCTCTCCGAGTGGG 1559
QY 1600 GAGTCCGCTGGTAACGTGTATTCTGACCGTCCGCTGCTTTCATGTGGACCTGTGTGC 1659
DB 1560 GAATCCCGTGGCTGACGTGTCTTGACCGTCCGCTGCTTCAATGGCGCACCTGTGTGA 1619
QY 1660 GGGACTGCTGCCCGAAACCGGGTTCGTTAGATTCCCTTTCCATFCGCTGCGCACGGGGC 1719
DB 1620 GGGACTGCTGCCCGAGACCGGGTCGTTAGTTCCCATTCATCCATCGTGGCGGTGGGC 1679
QY 1720 CTCGGCTGACAAAGACTTGAAGCTGTGCCCTTCGCTCAACAGGACAACCTCCCTTCACCA 1779
DB 1680 CTCGGCTGACAAAGACTTGAAGCTGTGCCCTTCGCTCAATAGGACAACCTCCCTTCACCA 1739
QY 1780 TAAGGGGCCCTGGGCAACACAGGGAGAGGCAACCCGGTGCCTGCGCTTGGGTTTG 1839
DB 1740 TTAGGGGCCCTGGGCAACACAGGGCGAGGCAACCCGGTGCCTGCGCTTGGGTTTG 1799
QY 1840 GGTCTACACCATGACCAAGATCCGGATTCCCTGCAATTTGGTGAATGTCCCAACACAG 1899
DB 1800 GGTCTACGCCATGACCAAGATCCGAGATACCCATACATCTGTTGGTGTCCCAACACAG 1859
QY 1900 CCATAGAGCTCCGACTGGACGTTCCGGTCTTCCCGGAGTCCCGCCCATTAACAACT 1959
DB 1860 CCATGAGCTCCGACCGGAGCTTGGGTTCTTCCCGGAGCCCGCCCTCTCAACAACT 1919
QY 1960 GCATGCGGCTAGGCACGGAAGTGTCTGAGGCATTGGCGGAGCTGGGCTTACGGGGGGT 2019
DB 1920 GCATGCTCTTGGGCACGGAAGTGTCCGAGGCACTTGGGGGGCTGGCTCACGGGGGGT 1979
QY 2020 TCTAGGAGCTCTGGTTCGCAAGTGTTCGAGCTGTAGGACGCCGAAATCCGGTTTGGC 2079
DB 1980 TCTATGAACCCCTGGTGCAGAGTGTTCGAGCTGTATGGGAAGCCGAAATCCGGTTTGT 2039
QY 2080 CGGGTAGCATGCTGTCCTGCTAGACTGACGGTTCATACAGTCCAGGGGACCC 2139
DB 2040 CGGGTTGCAATGCTCTTCTGGGCGAGGCTGATGGGTTTATACATGTCAGGGTCACT 2099
QY 2140 TGCAGGAGTGGATTCGGGCAACTTCATCCCTCCCTCACGCTGGTGTCTCTTGGATTG 2199
DB 2100 TGCAGGAGTGGATGCAAGCAACTTCATCCCGCCCCCGCTGCTCTTGGACTTG 2159
QY 2200 TATTGTCTCTCTATCTATGATGAGCTGGCTGAGGACAGGTTGGTCCGTTGATCTGC 2259
DB 2160 TATTGTCTCTTATCTATGATGAGCTGGCTGAGGACAGGTTGGTCCCGCTGATCTGC 2219
QY 2260 TTCTGCTGTGTGTGGTGAACAGTGTGGGTTCTAGGACTCCGCGCTGGGACGCTG 2319
DB 2220 TGCTGTATGTTGGTGGTGAACAGCTGGCAGTCTTAGGGCTCCCGCTGTGGAACCG 2279
QY 2320 CCGTGGCGGTTGAAGTTTTCGGGCGCTGCTCTGTCATGCTGTGTGGGCTTCCCACTG 2379
DB 2280 CCGTGGCAGGTGAGTCTCTCCGCGGCCCTGCCCTGTCTGCTGTGCTGGGACTCCCGTGC 2339
QY 2380 TCAGTATGATACTAGGTCTAGCAAAACCTGGTGTGTGTACTTTCGCTGGATGGGCCCTCAGC 2439

DB 2340 TCAGTATGATAATTGGGTTTGGCAAAACCTGCTGCTGTACTTTAGATGTTGGAGCCCAAC 2399
QY 2440 GCCTCATGTTCCCTCGTGTGTGGAAGCTCGCTCGGGAGCTTCCCGCTGGCACTTTGA 2499
DB 2400 GCCTGATGTTCCCTCGTGTGTGGAAGCTTCTCGGGAGCTTCCCGCTGGCCTCTTGA 2459
QY 2500 TGGGGATTTTCGGGACCCCGGGCGCACCTCTGTGTCGGGGCGGAGTTCCTGCTTCGATG 2559
DB 2460 TGGGGATTTTCGGGACCCCGGGCGCACCTAGTCTCGGGCGGAGTTCCTGCTTCGATG 2519
QY 2560 TCACATTCGAGGTGGACACTTCCTGCTGTGGCTGGGTGGGTGGCCAGCGTGGTGGCTTGGG 2619
DB 2520 CTACATTCGAGGTGGACACTTCCTGCTGTGGCTGGGTGGGTGGCCAAATGTGCTAGCTGGG 2579
QY 2620 CCATAGCGCTCTGAGCTCAATGAGCGCAGGGGGTGGGAAGCACAAAGCCGTGATCTATA 2679
DB 2580 CCATTCGCGCTCTGAGCTCGATGAGCGAGGGGGTGGAGGCACAAAGCCGTGATCTATA 2639
QY 2680 GGACGTGTTTAAAGGTACAGGCTGTGCGCCAGAGGGTGGTCCGAGGCCCTCTCGGG 2739
DB 2640 GGACGTGTTTAAAGGTACCAGGCAATCCGTCAAGGGTGGTGGAGAGCCCTCTCGGG 2699
QY 2740 AGGGGCTCTCTACAAAGCTTCTGACGTTCCCTGCTGGTGGCTTCATACATCTGGCCGG 2799
DB 2700 AGGGGCGCTTGCACAAACCCCTGACCTTTGCCCTGGTCTGGCTCTGATCTGGCCAG 2759
QY 2800 ATGCTGTGATGATGGTGGTGGCTTGGCTTGGCTTCTCTCTTTGGCTTCTCGACGCGTTG 2859
DB 2760 ATGCTGTGATGATGGTGGTGGCTTGGCTTGGCTTCTCTCTTTGGCTTCTCGACGCGTTG 2819
QY 2860 ACTGGGCCCTGGAGGAGCTCTCTGCTCTCCCGGCCCTCGTTTACGGCGACTGGCAGCGGTG 2919
DB 2820 ATTGGGCCCTGGAGGAGATCTTGGTGTCCCGGCCCTCGCTGCGGCGCTTGGCTCGGGTG 2879
QY 2920 TTGAGTCTGTGTGATGGCGGGCGAGAAGCCACCACTCCAGCTGGCTTCCAAAGATGT 2979
DB 2880 TTGAGTCTGTGTGATGGCGGGTGAAGAGCCACAAACCGCTCCGCTGGCTTCCAAAGATGT 2939
QY 2980 GCGCAAGAGGGGCTACTCTTTGACCACATGGCTCTTCTCGCGGCTGTCAAGGAGC 3039
DB 2940 GTGGAGAGAGGCTTATTTCTGATCATATGGCTCATTTTCCGCTGCTGTCAAGAGC 2999
QY 3040 GCTTGTGGAATGGAGCGCGCTTTGGAGCCCTTGTCAATTCATCTAGACGAGCTGTGCA 3099
DB 3000 GCTTGTGGAATGGAGCGCGCTTGTCAACCTCTGTCTATTCATCTAGACGAGCTGTGCA 3059
QY 3100 TCATCAGAGATGCCGCGAGGACCTGTCTCTGGGACAGTCCGCTCATGGGTTTACCCGTG 3159
DB 3060 TCATACGGGATGCCGCGAGGACTTTGTCTTCCGGGCAATCGCTCATGGGTTTACCCGTG 3119
QY 3160 TAGCACGGCGGCTGATGAGGTTCTCATCGGCGTCTTTCAGGATGTGAATCATTTGGCTC 3219
DB 3120 TTGGCGCCCTGGTATGAGGTTCTCATCGGCGTCTTCCAGGATGTGAATCATTTGGCTC 3179
QY 3220 CCGGTTTGTCCGACTGCAACAGTGTGTATCCGCTGGGTGCGGAAAGGGTTCCTCGGGG 3279
DB 3180 CCGGTTTGTTCGACCGCGCTTGTGTCTATCCGACGCTGGGTCGGAAGGGCTTCTTGGGG 3239
QY 3280 TCAGGAAGGCGAGCTTTCACAGTAGGATCCTGACTTACATCCAGGAAGCTCATGGTGT 3339
DB 3240 TCACAAAGGCTGCTTGACAGGTCCGGATCCTGACTTACATCCAGGAAGCTCATGGTGT 3299
QY 3340 TGGGAGCGGCTAGCTACGAAGCATGGGCACATGCTCTGAATGGCTCTCTTCCAACTT 3399
DB 3300 TGGGAGCGCTAGCTCCGGAAGCATGGGAACATGCTTGAACGCCCTGCTTCCAGGACT 3359
QY 3400 TCCATGGGGCTCATCCCAACCATCCGCCAGCCCGTGGGGGGCCCTTAATCCAGGTGGT 3459
DB 3360 TCCATGGGGCTCATCCCAACCATCCGCCAGCCCGTGGGGGGCCCTTAATCCAGGTGGT 3419
QY 3460 GGTACAGCTGATGAGTTCACGCTTACCCGCTTCCAGATGGGCAACTTCGTTGACGC 3519

Db 3420 GGTACGCAGTGATGATCATCGGTGTATCCACTCCCGGATGGGCTACTTCGTTAAAGC 3479
Qy 3520 CTTGACATTCGACGCGAGTCCCTGTTGGGTATTATAGATCCGACGCGGCTTTGTGCCATG 3579
Db 3480 CTTGTACTTCGACAGGCTGAGTCCCTGTTGGGTATCATGATCCGACGGGCGCCTATGCCATG 3539
Qy 3580 GCTTGAGCAAGGGGACAAAGTTGAGCTGAGTGTGGCCATGAGAGTCTCTGACTTTCCGTTG 3639
Db 3540 GCTTGAGCAAGGGGACAAAGTTGAGCTGAGTGTGGCCATGAGAGTCCCTGATTTCCGCTG 3599
Qy 3640 GTTGGTCTGCTGTTACCCGCTCTTTGCGACAAAGGCGACGACAGTAAAGATGCTGTTGTCAG 3699
Db 3600 GCTG 3659
Qy 3700 TGCTCCACTCTGCGGCGAGGTTACTGCGCGCGCGATTCACCTAGGCGCTGGACTCAAGTAC 3759
Db 3660 TGCTTCACTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3719
Qy 3760 CAACAGATGCCAAAGACTACACAGAACCCCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3819
Db 3720 CAACAGATGCCAAAGACTACACAGAACCCCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3779
Qy 3820 AGGCCCCCTGTTATGCTTACGCGGCGGGAAGAGACACCGCTACCGCTTGAGTACG 3879
Db 3780 AGGCCCCCTGTTATGCTTACGCGGCGGGAAGAGACACCTCGCGTCCCGTGGAGTACG 3839
Qy 3880 GCAACATGGGCGACAAAGTCTTGATCTTGAACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3939
Db 3840 GCAACATGGGCGACAAAGTCTTGATCTTGAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 3899
Qy 3940 GCCCATACATGAGGCGCTGCGGGGGAACACCCCGATTTACTGTGGCCATGACACCA 3999
Db 3900 GCGCGTACATGAGCGGCTGCGGGGTAACATCCAAAGTATATACTGTGGCATGATACAA 3959
Qy 4000 CTGCTTTACAAAGATCACTGACTGCGCCCTTACGATTTCCACTTTACGGAAGTTTTGG 4059
Db 3960 CTGCTTTACAAAGATCACTGACTGCGCCCTGACCTATTTCAACCTATTTGGAGGTTTTGG 4019
Qy 4060 CCAACCTTAGCAGATGCTGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4119
Db 4020 CCAACCTTAGCAGATGCTGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4079
Qy 4120 ATGACTCAACTGTGTTGGGCAATTTGGGCGTGTGAGGAGTGGCGGAGGATGTGGAG 4179
Db 4080 ATGACTCAACTGTGTTAGGCAATTTGGGAGGTTGCGGAGTGGCGGTGGTGGCGAG 4139
Qy 4180 TGCAATTTGGTGTCTACGCCACTGCCACCCCTCCGCGATCCCGGATACCCAGACCCAT 4239
Db 4140 TGCAATTTGGTGTCTACGCCACTGCCACCCCTCCGCGATCCCGGATACCCAGACCCCT 4199
Qy 4240 CAATCATTGAGACAAACTGGACGTTGGGAGAGATCCCTTCTATGGGCATGGCATACCTC 4299
Db 4200 CAATCATTGAGACAAACTGGACGTTGGGAGAGATCCCTTCTATGGGCATGGCATACCTC 4259
Qy 4300 TTGAGCGGATGGGACCGGAGGATCTGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4359
Db 4260 TCGAGCGGATGGGACCGGAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4319
Qy 4360 GCTGGCGGGCGAGTTTTCGCTAGGGGGTAAATGCCATGCCCTATTACAGGGGGAAG 4419
Db 4320 GCTTGTCTGGCGAGTTCTCCGCTAGGGGGTCAATGCCATTTGCCATTTATAGGGGTAAG 4379
Qy 4420 ACAGTTCTATCATCAAGATGGAGACCTGGTGGTGTGCTACAGACGCACTATCCACTG 4479
Db 4380 ACAGTTCTATCATCAAGATGGGACCTGGTGGTGTGCTGCTACAGACGCACTATCCACTG 4439
Qy 4480 GGTACACTGGGAACCTTCGATCTGTCACCGATTTGGGCTTAGTGGTGGAGAGTCTGCTG 4539
Db 4440 GGTACACTGGGAATTTTCACCTCCGCTACCCGACTGTGGATTTAGTGGTGGAGAGTCTG 4499
Qy 4540 AGGTGACCTTTGATCCCACTATACCATCTCCCTGCGACGCTGCCCGCTGGCTGAAC 4599
Db 4500 AGGTGACCTTTGATCCCACTATACCATCTCCCTGCGGACAGTGCCTGCGTGGCTGAAC 4559

Qy 4600 TGTGATCAGCGGCGAGGACGACCGGTAGGGCAGGTCTGGGCGCTACTACTACGCGG 4659
Db 4560 TGTGATCAGCGGCGAGGACGACCGGTAGGGCAGGTCTGGGCGCTACTACTACGCGG 4619
Qy 4660 GGGTGGCAAGGCCCTGCTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 4719
Db 4620 GGGTGGCAAGGCCCTGCTGGGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 4679
Qy 4720 CCGGTGTGACCTGGTACGGAATGGAACTGACCTGACAGCAAACTACTGAGACTTTAGC 4779
Db 4680 CTGGAGTGACCTGGTACGGAATGGAACTGACCTGACAGCAAACTACTGAGACTTTAGC 4739
Qy 4780 ACAATGCGCCCTTACACCGCAGCGCTGACATTTGGGGAAGCCGCTGTTCTTTT 4839
Db 4740 ACGACTGCGCTTACACCGCAGCGCTGCGGCTGATATCGGAGAACCGGCTGTTCTTCT 4799
Qy 4840 CGGGCTTGGCCCGTTGAGGATGATCCGATGTTAGTGGGCAAAAGTTGCGGCGGTCA 4899
Db 4800 CTGGCTGCGCCCTTACACCGCAGCGCTGCGGCTGATATCGGAGAACCGGCTGTTCTTCT 4859
Qy 4900 ACTGGCCCTTCTGCTGGTGTGCTGAGCGACCATGTCGGGGAACACTGCTCCCGGCC 4959
Db 4860 ACTGGCCCTTCTGCTGGTGTGCTGAGCGACCATGTCGGGGAACACTGCTCCCGGCC 4919
Qy 4960 CATCGEATGACCCCGCTGCGGCGAGTCTGAAAGGCGCCGAATCCTGTCACACTCTCTGTA 5019
Db 4920 CATCGEATGACCCCGCTGCGGCGAGTCTGAAAGGCGCCGAATCCTGTCACACTCTCTGTA 4979
Qy 5020 GGTGGGCAATGATTTACCATCTAAAGTGGCGGCGCATCACATCGTGACACCTGGTCC 5079
Db 4980 GGTGGGCAATGATTTACCATCTAAAGTGGCGGCGCCACACATAGTGACAGACCTGGTCC 5039
Qy 5080 GTAGCTCGGGTGGCGGAGGTTACGTCCTGCGATGCGGAGCCCATCTTGTGATGGTG 5139
Db 5040 GGAGACTCGGTGTGGCGGAGGTTACGCGCGCTGCGGAGCTGGGCGCATCTTGTGATGATCG 5099
Qy 5140 GCCTCGCTATTGCGGGGCGCATGATCTATGCTCATACACGGGTCTCTGCTGGTGGTTA 5199
Db 5100 GTCTAGCTATTGCGGGGGGAATGATCTAGCGCTCATACACGGGTGCTGATGTTGGTGA 5159
Qy 5200 CAGACTGGGATGTGAAGGGGGTGGCAGCCCCCTTTATCGGCATGGAGACACGACGCG 5259
Db 5160 CAGACTGGGATGTGAAGGGGGTGGCAGCCCCCTTTATCGGCATGGAGACACGACGCG 5219
Qy 5260 CCCAGCCGTTGTGACAGTCCCGCTGAGCCATCGCGCGGGGGAGAGTCTGCGCCAT 5319
Db 5220 CTCAGCCGTTGTGACAGTCTCTCGGTGAGACCATCGCGCGGGGGTGAATCAGCACCAT 5279
Qy 5320 CGGATGCCAACACAGTACAGATGCGGTGGCGGCATCCAGGTGATTCGATTTGTCAG 5379
Db 5280 CGGATGCCAACACAGTACAGATGCGGTGGCGGCATCCAGGTGATTCGATTTGTCAG 5339
Qy 5380 TCATGACCTGTGCTGCGGGAAGTGTCTCTTGGCCCGAGGCTAAGACGCGCGAGGCT 5439
Db 5340 TCATGACCTGTGCTGCGGGAAGTGTCTCTTGGCTCAGGCTAAGACGCGCGAGGCT 5399
Qy 5440 ACGAGCTTACACCAAGTGGCTTGTGGTGTCTACACGGGAGCGGGCGCTGCCACTG 5499
Db 5400 ACACAGACGCCAACGTTGCTGCTGCTGCTGCTATACGGGAGCGGGCGCTTCCACTG 5459
Qy 5500 TTTCAATTTGTGACAGCTCTTTCGCGGGGCTGGCGGCGGTGAGGCCATTCGCACA 5559
Db 5460 TATCATTTGTGACAGCTCTTTCGCGGGGAGGCTGGCGGCTGTTGGGCCATTTGCCACA 5519
Qy 5560 GTGTAATAGCTGCGGAGTGGCGGCTATGGGCTTCTAGGAGCCCTCCATTTGGCTGTG 5619
Db 5520 ACGTATTTGCTGCGGCTGGCGGCTACGGGCTTCAAGAGCCCGCTGTTGGCAGCG 5579
Qy 5620 CCGCTTCTACCTCATGCGGTTGGCGCTGCGGAGCAACCGCAACCCGCTTTAGCTCCG 5679
Db 5580 CCGCTTCTACCTCATGCGGTTGGCGCTGCGGAGCAACCGCTCAGACGCGCTTGGCATCTG 5639

Db 7800 AGGCCCCCGCCTCATTTGTTTCCCGCCCTGGACTTCGGATAGCTGAAAAAGCTCATCT 7859
QY 7900 TGGGAGACCTCGACGGGTAGCAAGGGGTGTTGGGGGGGCGCTACGCCCTTCCAGTACA 7959
Db 7860 TGGGAGACCCAGACCGGTAGCAAGGGGTGTTGGGGGGGCGCTACGCCCTTCCAGTACA 7919
QY 7960 CCCCAAATCAGGAAATAGGAGATGCTCAAACTGTGGGAATCAAGAAGACACCATCGG 8019
Db 7920 CCCCAAATCAGGAGTTAAGGAGATGCTCAAGCTATGGAGGCTAAGAAGACCCCTTGG 7979
QY 8020 CCATCTGTGTGACGCCACATGCTTCGACAGTAGCATAACTGAAGAGACGTGGCGCTGG 8079
Db 7980 CCATCTGTGTGACGCCACCTCTTCGACAGTAGCATAACTGAAGAGACGTGGCTTGG 8039
QY 8080 AGACAGAGCTTTATGCGCTGGCTTCAGACCATCCAGAAATGGTGGTGGGAAAT 8139
Db 8040 AGACAGAGCTGTACCGCTCTGGCCCTCTGACCATCCAGAAATGGTGGGACACTTGGGAAAT 8099
QY 8140 ACTATGCCCTCTGGCAACAATGGTAAACCCCGAGGGGTGCCAGTGGGTGAGAGGTATTGTA 8199
Db 8100 ACTATGCCCTCAGCACCATGGTCAACCCGGAAGGGTGCCCTCGGTGAGAGGTATTGCA 8159
QY 8200 GATCCTCAGGGTCTTGACCAACCATGGAGCAACTGCTTGACTTGTCTATATCAAGGTGA 8259
Db 8160 GATCCTCGGGTGTCTAAACAACCTAGCGGAGCAACTGCTTGACCTGCTACATCAAGGTGA 8219
QY 8260 AAGCGCCTGTGAGAGGTGGGGCTGAAAAATGTCGCTCTCATCGCTGCGATGACT 8319
Db 8220 AAGCGCCTGTGAGAGGTGGGGCTGAAAGATGTCTCTCTCATAGCCCGCGATGACT 8279
QY 8320 GTTGTGATCATATGCGAAGCGCTGTGCGATCTTAGCGACCTTTGGCGAGAGCCCTGG 8379
Db 8280 GCTTGTGATCATATGCGCGGCCAGTGTGCGACCCAGCGACGCTTTGGCGAGAGCCCTAG 8339
QY 8380 CGAGCTACGGGTACGATCGCGAGCCCTCGTATCATGCAATGAGACAGCGCCCTCTCT 8439
Db 8340 CGAGCTATGGGTACGCGTCCGAGCCCTCATATCATGCAATGAGACAGCGCCCTCTCT 8399
QY 8440 GCTCCACTGGCTAGCTGAGTGCATGAGATGCAGATGGGAAGCCCATTTCTTCCAGCACGG 8499
Db 8400 GCTCCACTGGCTAGCTGAGTGCATGAGATGCAGATGGGAAGCCCATTTCTTCCAGCACGG 8459
QY 8500 ACTTTCGGAGGCCCTCGCTCCATGTGCGAGCGGTACAGTGACCAATAGCTTCCGCGCA 8559
Db 8460 ACTTCCGGAGGCCCTCGCTCCATGTGCGAGTGTAGTACCGGATGGTTCGCGCA 8519
QY 8560 TCGGTTACATCTCTATACCCCTTGGCATCTTATACAGAGGTGGGTCAATCATCCCTCAG 8619
Db 8520 TCGGTTACATCTCTCTTATCTTGGCACCCCATCACAGGTGGGTCAATCATCCCTCAG 8579
QY 8620 TCGTACCTCGCGGTTTAGGGGTGTGGCACACCGCTCTGATCTGTGTTGCCAGGTAC 8679
Db 8580 TCGTACCTCGCGGTTTAGGGGTGTGGCACACCGCTCTGATCTGTGTTGCCAGGTAC 8639
QY 8680 ATGGTAATTAATACAAAGTTTCCACTGGACAACTGCCTAACATCATCGTGGCCCTCCAG 8739
Db 8640 ATGGTAATTAATACAAAGTTTCCACTGGACAACTGCCTAACATCATCGTGGCCCTCCAG 8699
QY 8740 GACACGACGCTTGAGGGTTACCGCAGACACAACTAAGACAAAATGGAGGCTGGCAAG 8799
Db 8700 GACACGACGCTTGAGGGTTACCGCAGACACAACTAAGACAAAATGGAGGCTGGTAAG 8759
QY 8800 TCGTCAGGACCTCAAGCTCCCTGCGCTAGCAGTACCCGGAAGAGCCCGGGCATTCG 8859
Db 8760 TCTGAGGACCTCAAGCTCCCTGCGCTAGCAGTACCCGGAAGAGCCCGGGCGTTGC 8819
QY 8860 GAACGCTATGCTCCGGTTCGCGGTTGGGCTGAGTGGCTAGGGGCTGTTGTGGCGCT 8919
Db 8820 GAACGCTATGCTCCGCTCGCGGTTGGGCTGAGTGGCTAGGGGCTGTTGTGGCATC 8879
QY 8920 CAGGCTCGGGTTCCTCCCTCCGAGATTGCTGGTATCCCCGGGGTTTCCCGCTTCC 8979
Db 8880 CAGGCTACGGCTTCTCCTCCCTCGAGATTGCTGGTATCCCGGGGGTTTCCCTCTCTCC 8939

QY 8980 CCCCTATATGGGTGGTTTCATCAATTGATTTCACAAAGCCAGAGGAGTCCGTGGCGGT 9039
Db 8940 CCCCTATATGGGTGGTTTCACCAATTTGATTTTACAAGCCAGAGAGTCCGTGGCGGT 8999
QY 9040 GGTGGGGTCTTAGCCCTGCTCATCGTAGCCCTCTTCGGGTGAACATAAATTCATCTGTT 9099
Db 9000 GGTGGGGTCTTAGCCCTGCTCATCGTAGCCCTCTTCGGGTGAACATAAATTCATCTGTT 9059
QY 9100 GGGCAAGTCCGGTACTGATCATCACTGGAGAGGTTCCCGCCCTCCCGCCCGCAGGG 9159
Db 9060 GGGCGAGGTCGTGGTACTGATCGTCAACCGAGAGGTTCCCGCCCTCCCGCCCGCAGGG 9119
QY 9160 GTCTCCCGCTGGGTAAAGAGCCGCTTGGGAGGATGTTGTTACTTAACCCCTG 9219
Db 9120 GTCTCCCGCTGGGTAAAGAGCCGCTTGGGAGGATGTTGTTACTTAACCCCTG 9179
QY 9220 GCAGGTCACAAAGCCCTGATGGTCTAATGCACATGCCACTTCGGTGGCGGTCCGTACCTTA 9279
Db 9180 GCAGGTCACAAAGCCCTGATGGTCTAATGCACATGCCACTTCGGTGGCGGTCCGTACCTTA 9239
QY 9280 TAGCTAATCCGTGACTAGGGCTGCTCGCAGAGCCCTCCCGGATGGGGACAGTGCAC 9339
Db 9240 TAGCTAATCCGTGACTAGGGCTGCTCGCAGAGCCCTCCCGGATGGGGACAGTGCAC 9299
QY 9340 TGTGATCTGAAGGGTGCACCCCGGTAA 9367
Db 9300 TGAGATCTGAAGGGTGCACCCCGGAA 9327

RESULT 13

AA02517

ID AA02517 standard; cDNA: 9327 BP.

AC AA02517;

DT 06-MAY-1999 (first entry)

XX US856134 Seq ID 234.

XX Non-A Non-B Non-C Non-D Non-E Hepatitis Virus; immunogen; HGV; HBV; immunoreactive; serum alanine aminotransferase; hepatitis A virus; HCV; hepatitis B virus; hepatitis C virus; hepatitis D virus; HDV; HBV; hepatitis E virus; Flaviviridae; prophylactic; therapeutic; diagnosis; antibody; vaccine; detection; ds.

OS Hepatitis G virus.

XX US856134-A.

XX 05-JAN-1999.

XX 05-JUN-1995; 95US-0461361.

XX 19-MAY-1995; 95US-0444733.

XX 20-MAY-1994; 94US-0246985.

XX 03-AUG-1994; 94US-0285543.

XX 03-AUG-1994; 94US-0285558.

XX 03-AUG-1994; 94US-0285561.

XX 26-OCT-1994; 94US-0329729.

XX 23-NOV-1994; 94US-0344271.

XX 16-DEC-1994; 94US-0357509.

XX 15-FEB-1995; 95US-0389886.

XX 05-JUN-1995; 95US-0461361.

XX (GENE-) GENELABS TECHNOLOGIES INC.

XX Fry KE, Kim JP, Linnen JM, Wages J, Young LM;

XX WPI: 1999-105108/09.

XX New isolated hepatitis G virus antigens - used to develop products for the diagnosis, prophylaxis and therapy of hepatitis G virus

PT infections
xx
PS Example 18; Column 337-346; 204pp; English.
xx
CC This invention describes a Non-A Non-B Non-C Non-D Non-E Hepatitis Virus
CC (HGV) immunogenic composition which comprises a purified HGV polypeptide
CC antigen at least 10 amino acids in length which is specifically
CC immunoreactive with HGV-positive sera, present in a carrier, where HGV
CC is characterised by (a) production of elevated serum alanine
CC aminotransferase levels in an infected primate (b) its serological
CC distinction from hepatitis A virus (HAV), hepatitis B virus (HBV),
CC hepatitis C virus (HCV), hepatitis D virus (HDV), and hepatitis E virus
CC (HEV) (c) membership in the virus family Flaviviridae. The compositions
CC can be used to develop products useful for prophylactic, therapeutic and
CC diagnosis applications. The immunogenic compositions can be used for the
CC production of antibodies, in vaccines and for detection and diagnosis.
xx
xx Sequence 9327 BP; 1682 A; 2532 C; 2984 G; 2129 T; 0 other;
SQ

Query Match 83.9%; Score 7885.6; DB 20; Length 9327;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 8433; Conservative 0; Mismatches 894; Indels 1; Gaps 1;

Qy 40 GCAAGCCCAATAACCGACGCTATCTAAGTAGACGCAATGACTCGGCGGACTCGGCG 99
Dy 1 GCAAGCCCAATAACCGACGCTATCTAAGTAGACGCAATGACTCGGCGGACTCGGCG 60
Qy 100 ACCGGCCAAAAGGTGGTGGATGGGTGACAGGGTGGTAGGTGCTAAATCCCGGTGAT 159
Dy 61 ACCGGCCAAAAGGTGGTGGATGGGTGATGACAGGGTGGTAGGTGCTAAATCCCGGTGAT 120
Qy 160 CCTGGTAGCCACTATAGTGGGTCTTAAGAGAGGTCAAGACTCTCTTGTGCTGGCGG 219
Dy 121 CTGTGTAGCCACTATAGTGGGTCTTAAGAGAGGTTAAGATTCCTCTGTGCTGGCGG 180
Qy 220 GAGACCGGACGCTGACAGGTGCTGGCCCTACCGGTGTGAATAAGGGCCGACGTGAC 279
Dy 181 GAGACCGGACGCTGACAGGTGCTGGCCCTACCGGTGTGAATAAGGGCCGACGTGAC 240
Qy 280 GCTGCTGTTAAACCGAGCCGTCACCCACCTGGGCAACAGCCGCCACGTACGGTCCAC 339
Dy 241 GCTGCTGTTAAACCGAGCCGTTACCCACCTGGGCAACAGCCGCCACGTACGGTCCAC 300
Qy 340 GTCGCCCTTCAATGCTCTCTTGACCAATAGTGTATATCCGCGAGTGTGACAAGACCACT 399
Dy 301 GTCGCCCTTCAATGCTCTCTTGACCAATAGGCGTAGCGGAGATTGACAAGACCACT 360
Qy 400 GGGGCGCGGGGGTATGGGGAAGGACCCCAACCCCTGCCCTTCCGGTGGGCGCGGAAAT 459
Dy 361 GGGGCGCGGGGGCT-TGGAGAGGAGACTCCAAGTCCCGCCCTTCCCGGTGGGCGCGGAAAT 419
Qy 460 GCATGGGCGCACCCAGCTCCGCGCGGCTGACGCGGGGTAGCCCAAGAAATCCTTCGGG 519
Dy 420 GCATGGGCGCACCCAGCTCCGCGCGGCTGACGCGGGGTAGCCCAAGAAATCCTTCGGG 479
Qy 520 TGAGGGGGGTGGCATTTCTCTTTTATACCATCATGCGAGTCTCTCTGCTCTCTCG 579
Dy 480 TGAGGGGGGTGGCATTTCTCTTTTATACCATCATGCGAGTCTCTCTGCTCTCTCG 539
Qy 580 TGGTTAGGCGCGGGGCATTTCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 639
Dy 540 TGGTTAGGCGCGGGGCATTTCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 599
Qy 640 ATTTCTTCACAAATGCTGTGTCGCCCGGAAGACATCGGGTCTGCTGGAAGGGGATGCC 699
Dy 600 ATTTCTTCACAAATGCTGTGTCGCCCGGAGGACATCGGGTCTGCTGGAAGGGGATGCC 659
Qy 700 TGGTGGCCCTGGGTGGACGCTTTGACACCGCTTGTGCTGGCCACTGTATCAGCGGGTT 759
Dy 660 TGGTGGCCCTGGGTGGACGCTTTGCACTGACCAATGCTGGCCACTGTATCAGCGGGTT 719
Qy 760 TGGCTGTGCGGCTTGGCAAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 819
Dy 720 TGGCTGTGCGGCTTGGCAAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 779

Db 720 TGGCTGTGCGGCTTGGCAAGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 779
Qy 820 GGCCCTTGTGCGGCTTACGCTAGCCGCGGATCCCTGGGCTCTGGGCGAGGCTTACTCCG 879
Dy 780 GGCCCTTGTGCGGCTTACGCTAGCCGCGGATCCCTGGGCTCTGGGCGAGGCTTACTCCG 839
Qy 880 GGCTCTTACAGCTTGGTGGTGGTGGGCGCGGGTCTACCTGATGCCCACTGAAGT 939
Dy 840 GTGTCTTACCGTGGGAGTCCGCTTACGCGCGGAGTCTACCGGCTCCCTAACCTGACGT 899
Qy 940 GTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 999
Dy 900 GTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 959
Qy 1000 CTTCCAAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1059
Dy 960 CTTCCAAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1019
Qy 1060 TGATGAGCCTGACCCCTCTCTTGGTGGTGGCGGCAATTCCTTTGCTGGAGCAACGGA 1119
Dy 1020 TGATGAGCCTGACCCCTCTCTTGGTGGTGGCGGCAATTCCTTTGCTGGAGCAACGGA 1079
Qy 1120 TTGTGATGGTCTTCTCTGCTGCTGACGATGGCGGGATGTTGCAAGGCGGCGGCGGCTCCG 1179
Dy 1080 TTGTGATGGTCTTCTCTGCTGCTGACGATGGCGGGATGTTGCAAGGCGGCGGCTCCGCTCCG 1139
Qy 1180 TTTTGGGCTCCGCGGCTTCTGCTGCTGACGATGGCGGGATGTTGCAAGGCGGCGGCTCCG 1239
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Dy 1200 ACGGTGGCTTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1259
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Dy 1320 GTGACCCCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1379
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Dy 1380 ATGTCTATGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1439
Qy 1480 CCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1539
Dy 1440 CCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1499
Qy 1540 GCACCATAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1599
Dy 1500 GCACCATAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1559
Qy 1600 GAGTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1659
Dy 1560 GAGTCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1619
Qy 1660 GAGTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1719
Dy 1620 GAGTCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1679
Qy 1720 CTGCGCTGACAAAGGACTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1779
Dy 1680 CTGCGCTGACAAAGGACTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1739
Qy 1780 TAAAGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1839
Dy 1740 TAAAGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1799
Qy 1840 GGTCTTACACCATGACCAAGATCCGCGGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1899
Dy 1800 GGTCTTACACCATGACCAAGATCCGCGGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1859

QY	2980	GGC	AA	GAG	GGC	CT	A	C	T	T	T	G	A	C	A	T	G	G	G	C	T	T	T	C	G	C	G	C	T	G	T	C	A	A	G	A	G	C	3039
DB	2940	GTG	C	A	G	A	G	A	G	C	T	T	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	2999		
QY	3040	G	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	3099			
DB	3000	G	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	3059				
QY	3100	T	C	A	T	C	A	G	A	T	G	C	C	G	A	G	A	C	C	T	G	T	C	T	G	G	A	C	C	T	G	T	C	T	G	3159			
DB	3060	T	C	A	T	A	C	G	G	A	T	G	C	C	G	A	G	A	C	C	T	G	T	T	T	T	T	T	T	T	T	T	T	T	T	3119			
QY	3160	T	A	G	C	A	C	G	C	G	T	G	A	T	C	A	G	T	T	C	A	T	C	A	T	C	A	T	C	A	T	C	A	T	C	3219			
DB	3120	T	T	G	C	G	C	G	T	G	A	T	C	A	G	T	T	C	A	T	C	A	G	A	T	G	T	C	A	T	C	A	T	C	A	3179			
QY	3220	C	G	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	3279					
DB	3180	C	G	G	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	3239					
QY	3280	T	C	A	A	A	G	C	A	G	C	T	T	G	A	C	A	G	T	A	G	G	A	T	C	A	T	C	A	T	C	A	T	C	A	3339			
DB	3240	T	C	A	A	A	G	C	T	T	G	A	C	A	G	T	A	G	G	A	T	C	A	T	C	A	T	C	A	T	C	A	T	C	A	3299			
QY	3340	T	G	G	A	C	G	C	T	A	C	G	A	A	G	C	A	T	G	C	A	T	G	C	A	T	G	C	A	T	G	C	A	T	G	3399			
DB	3300	T	G	G	A	C	G	C	T	A	C	G	A	A	G	C	A	T	G	C	A	T	G	C	A	T	G	C	A	T	G	C	A	T	G	3359			
QY	3400	T	C	A	T	G	G	G	C	T	T	C	A	C	A	C	A	T	F	G	C	C	A	C	A	T	F	G	C	C	A	C	A	T	3459				
DB	3360	T	C	A	T	G	G	G	C	T	T	C	A	C	A	C	A	T	F	G	C	C	A	C	A	T	F	G	C	C	A	C	A	T	3419				
QY	3460	G	G	T	C	A	G	C	A	G	T	C	A	G	C	T	A	C	C	G	T	T	C	C	A	G	A	T	G	G	G	C	A	T	3519				
DB	3420	G	G	T	C	A	G	C	A	G	T	C	A	G	C	T	A	C	C	G	T	T	C	C	A	G	A	T	G	G	G	C	A	T	3479				
QY	3520	C	T	G	C	A	T	T	G	C	A	G	C	A	G	T	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	3579				
DB	3480	C	T	T	G	A	T	T	G	C	A	G	C	A	G	T	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	3539				
QY	3580	G	C	T	T	C	A	A	G	G	G	A	C	A	A	G	T	T	A	G	C	T	T	G	G	C	A	T											

[illegible]

|||||
Db 8400 GCTCCACTTGGCTTGTAGTGAATGAGATGGGAAGGCCATTCTTCTCCTGACCAACGG 8459
QY 8500 ACTTTCGAGGCCCTCGCTCGCATGTGAGCGAGTACAGTACCACAAATGGCTTCGGCCA 8559
Db 8460 ACTTCGGAGGCGCTCGCTCGCATGTGAGTATAGTACCGCATGGCTTCGGCGCA 8519
QY 8560 TCGGTACATCTCTTATACCTTGGCTATCATACAGGTGGGTCAATCCCTCACG 8619
Db 8520 TCGGTACATCTCTTATACCTTGGCACCCCAATACAGGTGGGTCAATCCCTCAAG 8579
QY 8620 TGCTACCTCGCGCTTATAGGGTGGTGGCACACCGTCTGATCCTGTGTGGTGGCCAGGTAC 8679
Db 8580 TGCTACCTCGCATTCAGGGTGGAGGCACACCGTCTGATCGGTTTGGTGGCCAGGTAC 8639
QY 8680 ATGGTAATTAATACAAAGTTCACCTGGACAAACTGCTTAACATCATCGTGGCCCTCCAG 8739
Db 8640 ATGGTAATTAATACAAAGTTCACCTGGACAAACTGCTTAACATCATCGTGGCCCTCCAG 8699
QY 8740 GACGACGAGCTTGAAGGTTTACCGCAGACACAACTAAGACAAATGGAGGCTGGCAAG 8799
Db 8700 GACGACGAGCTTGAAGGTTTACCGCAGACACAACTAAGACAAATGGAGGCTGGTAAG 8759
QY 8800 TGCTAGCGACCTCAAGCTCCCTGGCTAGCATGCCAGGAAAGAGCGCGGGCATTCG 8859
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QY 8860 GAACGCTATGCTCCGCTCGCGGTTGGCTGAGTGGCTAGGCGGCTGTGTGGCGTC 8919
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QY 8920 CAGCGCTGCGGCTTCCGCTCCGAGATTGCTGTATCCCGGGGTTTCCCGCTTTCC 8979
Db 8880 CAGCGCTACGCTTCTCCGCTGAGATTGCTGTATCCCGGGGTTTCCCGCTTCC 8939
QY 8980 CCCCCATATATGGGGTGTTCATCAATTTGATTTCAAGCCAGAGAGTTCGCTGGCGGT 9039
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QY 9040 GGTGGGTCTTAGCCCTCTCATCTGATGCTGCTTCCGCTGCACTAAATTCATCTGT 9099
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QY 9220 GCAGGTCAAAGCTGATGTGCTAATGCACTGCCACTTCGGTGGCGGTCGCTACTTAA 9279
Db 9180 GCAGGTTAAAGCTGATGTGCTAATGCACTGCCACTTCGGTGGCGGTCGCTACTTAA 9239
QY 9280 TAGCGTAATCCGTAAGTACGGGTGCTCGCAGAGCCCTCCCGGATGGGCGACAGTGCAC 9339
Db 9240 TAGCGTAATCCGTAAGTACGGGTGCTCGCAGAGCCCTCCCGGATGGGCGACAGTGCAC 9299
QY 9340 TGTGATCTGAAGGGTGCACCCCGTAA 9367
Db 9300 TGATGATCTGAAGGGTGCACCCCGGAA 9327

RESULT 14
AAV82248
ID AAV82248 standard; cDNA; 9327 BP.
XX
AC AAV82248;
XX
DT 29-MAR-1999 (first entry)
XX
DE Hepatitis G virus clone 3ZHG-6.

XX
KW Hepatitis; HGV; diagnosis; vaccine; antigen; ds.
OS Hepatitis G virus variant PNF2161.
XX
PN US5849532-A.
XX
PD 15-DEC-1998.
XX
PF 06-JUN-1995; 95US-0464134.
XX
PR 19-MAY-1995; 95US-0444733.
PR 20-MAY-1994; 94US-0246985.
PR 03-AUG-1994; 94US-0285543.
PR 03-AUG-1994; 94US-0285558.
PR 03-AUG-1994; 94US-0285561.
PR 26-OCT-1994; 94US-0329729.
PR 23-NOV-1994; 94US-0344271.
PR 16-DEC-1994; 94US-0357509.
PR 15-FEB-1995; 95US-0389886.
PR 06-JUN-1995; 95US-0464134.
XX
PA (GENE-) GENELABS TECHNOLOGIES INC.
XX
PI Fry KE, Kim JP, Linnen JM, Wages J, Young LM;
XX
XX WPI; 1999-069731/06.
XX
XX Vector containing hepatitis G virus nucleic acid - and transformed
PT cells for producing recombinant HGV polypeptide
XX
XX Example 18; Column 337-346; 204pp; English.
XX
XX This is the nucleotide sequence of clone 3Z-HGV94-6, a near
CC full-length hepatitis G virus (HGV) genome produced by PCR
CC amplification (see AAV82242-47) of 3 overlapping segments of the
CC HGV variant PNF 2161 genome (see AAV82093) and cloning of PCR
CC products into vector pGEM32. This clone can be used to map the
CC various regions of the viral genome, study its replication, and
CC examine the mechanisms of HGV pathogenicity in human cells. The
CC invention provides a claimed vector that includes HGV-PNF 2161
CC nucleic acid and a method for the production of recombinant HGV
CC polypeptides (see AAV89452). These polypeptides can be used as
CC antigens (i) in diagnostic methods for detecting the presence of
CC HGV in test subjects, (ii) in vaccines, and (iii) in the
CC preparation of anti-HGV antibody.
XX
SQ Sequence 9327 BP; 1682 A; 2532 C; 2984 G; 2129 T; 0 other;

Query Match 83.9%; Score 7885.6; DB 20; Length 9327;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 8433; Conservative 0; Mismatches 894; Indels 1; Gaps 1;
QY 40 GCAAGCCCCATAAACGAGCCCTATCTAGTAGACGCAATGACTCGGCGCCGACGTCGGG 99
Db 1 GCAAGCCCCAGAAACCGAGCCCTATCTAAGTAGACGCAATGACTCGGCGCCGACGTCGGG 60
QY 100 ACCGGCCAAAAGGTGGTGGATGGGTGCACAGGTTGGTAGTCTGAATCCCGTCAAT 159
Db 61 ACCGGCCAAAAGGTGGTGGATGGGTGCACAGGTTGGTAGTCTGAATCCCGTCAAT 120
QY 160 CCTGTAGCCACTATAGTGGGTCTTAAGAGAAGGTCAAGACTCTCTTTGTGCCCTGCCG 219
Db 121 CTTGTAGCCACTATAGTGGGTCTTAAGAGAAGGTCAAGACTCTCTTTGTGCCCTGCCG 180
QY 220 GAGACGGCCACGGTCCACAGGTGCTGGCCCTACCGGTGTGAATAGGCCCGGACGTCAG 279
Db 181 GAGACGGCCACGGTCCACAGGTGCTGGCCCTACCGGTGTGAATAGGCCCGGACGTCAG 240
QY 280 GCTCGTCTGTTAAACCGAGCCCGCTACCCACCTGGGCAACACGACGCGCAGCTACGGTCCAC 339
Db 241 GCTCGTCTGTTAAACCGAGCCCGCTACCCACCTGGGCAACACGACGCGCAGCTACGGTCCAC 300

340 GTCCGCTTCAATGTCCTCTCTTGACCAATAGGTTTATCCGGGAGTTGACAGGACCAAGT 399
Db GTCCGCTTCAATGTCCTCTCTTGACCAATAGGTTTATCCGGGAGTTGACAGGACCAAGT 360
301 GTCCGCTTCAATGTCCTCTCTTGACCAATAGGTTTATCCGGGAGTTGACAGGACCAAGT 360
QY 400 GGGGGCCGGGGTTATGGGAGGAGGACCCCAAAACCTTGCCTTCCCGGTGGCGGGGAAAT 459
Db 361 GGGGGCCGGGGGT-TGGAGAGGAGTCCAAAGTCCCGCTTCCCGGTGGCGGGGAAAT 419
QY 460 GCATGGGGCACCCAGCTCCGGGGCCCTGCAAGCCGGGTAGCCCAAGAAATCCTTCGGG 519
Db 420 GCATGGGGCACCCAGCTCCGGGGCCCTGCAAGCCGGGTAGCCCAAGAAATCCTTCGGG 479
QY 520 TGAGGCGGGTGCCATTCTCTTTCTATACCAATATGCAAGCTTCTCTCTCTCTCG 579
Db 480 TGAGGCGGGTGCCATTCTCTTTCTATACCAATATGCAAGCTTCTCTCTCTCTCG 539
QY 580 TGGTTGAGCGGGGCCATTCTGGCCCCGGCCACACAGTGTGTCAGGCAATGGGCAAT 639
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QY 640 ATTTCTCTCAAAATTCGTGCCCCGGAAAGACATCGGTTCTGCCCTGGAAGCGGATGCC 699
Db 600 ATTTCTCTCAAAATTCGTGCCCCGGAGACATCGGTTCTGCCCTGGAAGGTGGATGCC 659
QY 700 TGGTGCCCTGGGGTGCAGGTTTGACCGGACCGTTGCTGGCCACTGTATCAGGCGGGT 759
Db 660 TGGTGCCCTGGGGTGCAGGTTTGACCGGACCGTTGCTGGCCACTGTATCAGGCGGGT 719
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Db 720 TGGCTGTGGGCTGGCAAGTCGGGGCCAGCTGTTGGGAACTGGGGAGCGCTGTACG 779
QY 820 GGCCCTTGTGCTCGGCTTAGTAGCGGGATCGTGGTCTGGGAGGTTTACTCGG 879
Db 780 GGCCCTTGTGCTCGGCTTAGTAGCGGGATCGTGGTCTGGGAGGTTTACTCGG 839
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Db 840 GTGCTCTAACGGTGGGAGTCGGCTTACGCGCGGATCTACCGGTCCTTAACCTGACGT 899
QY 940 GTGCACTAGAATGTGACGTTAAGTGGGGAAGTGAAGTTTGGAGATGACATGACGATGG 999
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QY 1000 CTTCCAAATCTGATTTGGATACCTTTGGAACTCCCATTTGAATTTGGAGAGGAG 1059
Db 960 CTTCCAACTACTGATTTGGAACTCTTGGAACTCCCATTTGAATTTGGAGAGGAG 1019
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QY 1120 TTGTCATAGTTTTCCTGCTGGTACGATGGCGGGAGTGTGAAGCGCCCCCGCTCCG 1179
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QY 1180 TTTTGGGGTCCCCCTTTGACTAGCGGTTGAAGTGGCAGTCATGCTCTGAGGGCTA 1239
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QY 1240 ACGGGTCCGGTATTTCCACTGGGGAGGAGTGGGATCGAGGGAATGTCACTCTTGT 1299
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QY 1300 GTGACTTGCCCCAACGGCCCTTGGGTTGGTCCCGCCCTTTTGGCAGGCGGTTGGGTGG 1359
Db 1260 GTGACTTGCCCCAACGGCCCTTGGGTTGGTGGTGGTGGTGGTGGTGGTGGTGG 1319
QY 1360 GCGACCCCATCACCATTGGAGCCAGGACAAACAGATGGGCCCTTATCATGCCGCCAAT 1419
Db 1320 GTGACCCCATCATTATTTGGAGCCAGGGCAAAATCAGTGGGCCCTTTATGCCCCAGT 1379
QY 1420 ATGTCATAGGCTGTGTCGGTAACGTGCGTGGGGTTCGGTGTCTTGGTTGCGCTCGA 1479

1380 ATGTCATAGGCTGTGTCATAGTCACTTGGGTGGGGTTCCGCTTCTTGGTATGCTCCA 1439
QY 1480 CCGGCGGTGCTGATTCGAAGATCGATGTGTGGAGTTTGGTCCGGTTGGATCTGCCAGCT 1539
Db 1440 CCAGTGTGCGGACTCGAAGATAGATGTGTGGAGTTTGGTCCAGTTGGCTCTGCCACCT 1499
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Db 1500 GCACCATAGCCGACTTGGATCATCGATCGCGACACGGTGGCTCTCCGAGTGGG 1559
QY 1600 GAGTCCCGTGGTAACTGTATTTCTGGACCGTGGCTGCTTTCATGTGGACACTGTGTGC 1659
Db 1560 GAATCCCGTGGTAACTGTATTTCTGGACCGTGGCTGCTTTCATGGGACACTGTGTGA 1619
QY 1660 GGGACTGCTGGCCCCAAGCCGGTTCGTTAGATTCCTTTCCATCGGTGGGACACGGGC 1719
Db 1620 GGGACTGCTGGCCCCAAGCCGGTTCGTTAGTTCCTTCCATCGGTGGGCTGGGC 1679
QY 1720 CTCGGCTGACAAAGACTTGGAACTGTGCGCTTCGTAACAGGACAACCTCCCTTCACCA 1779
Db 1680 CTCGGCTGACAAAGACTTGGAACTGTGCGCTTCGTAACAGGACAACCTCCCTTCACCA 1739
QY 1780 TAAGGGCCCCCTGGGCAACCAAGGGAGAGGCAACCCGGTTCGCGTCCCGCTGGGTTTG 1839
Db 1740 TTAGGGGGCCCCCTGGGCAACCAAGGGAGAGGCAACCCGGTTCGCGTCCCGCTGGGTTTG 1799
QY 1840 GGTCTACAGCATGACCAAGATCCGGGATTCCTGTCATTTGGTGAATGTCCACACACAG 1899
Db 1800 GGTCTACAGCATGACCAAGATCCGGGATTCCTGTCATTTGGTGAATGTCCACACACAG 1859
QY 1900 CCATAGAGCTCCGACTGGAACCTTCGGGTTCTTCCCGGAGTCCCGCCATTAACAAC 1959
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QY 1960 GCATGCGCTAGCACGGAAGTCTCTGAGGCAATTTGGCGGAGCTGGGCTTACGGGGGGT 2019
Db 1920 GCATGCTCTTGGCGCAGGAAGTCTCCGAGGCACTTTGGGGGGCTGGCTCACGGGGGGT 1979
QY 2020 TCTACAGGCTCTGTTGTCGAGGTGTTCGAGGTGTGAGGACCGCCAAATTCGGTTGCC 2079
Db 1980 TCTATGAACCCCTGTTGTCGAGGTGTTCGAGGTGTGAGGACCGCCAAATTCGGTTGTC 2039
QY 2080 CGSGGTACGATGGCTGCTCTGCTGAGACTTCACGCGTTTCATACGCTCCAGGCGAC 2139
Db 2040 CGSGGTTGCTGCTCTCTGCGGAGGCTGATGGGTTTATACATGTCAGGCTCACT 2099
QY 2140 TGCAAGAGGTGGATCGGCAACTTTCATCCCGCCCCGCGCTGCTTGGATTTG 2199
Db 2100 TGCAAGAGGTGGATCGGCAACTTTCATCCCGCCCCGCGCTGCTTGGATTTG 2159
QY 2200 TATTTGCTGCTATCTGATGATGAGTGGCTGGCTGAGGACCGGTTGGTCCGCTGCTGC 2259
Db 2160 TATTTGCTGCTATCTGATGATGAGTGGCTGGCTGAGGACCGGTTGGTCCGCTGCTGC 2219
QY 2260 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2319
Db 2220 TGTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2279
QY 2320 CCGTGGCGGTGAAGTTTTTGGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2379
Db 2280 CCGTGGCGGTGAGTCTTCGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2339
QY 2380 TCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2439
Db 2340 TCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2399
QY 2440 GCTCATGTTCT 2499
Db 2400 GCTCATGTTCT 2459
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Job time : 905 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 8, 2002, 23:18:15 ; Search time 6372 seconds
(without alignments)
19900.172 Million cell updates/sec

Title: US-09-828-498-1

Perfect score: 9395

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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5: em_estov:*
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7: em_estro:*
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11: gb_htc:*
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13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	56	0.6	1101	12	CNS017SY	AL108460 Drosophila
3	49.6	0.5	895	12	CNS0071A	AL066286 Drosophila
4	49	0.5	1100	12	CNS016KD	AL106855 Drosophila
5	48.6	0.5	934	12	AG080424	AG080424 Pan trogl
6	48.6	0.5	964	12	CNS003WG	AL065254 Drosophila
7	48	0.5	910	12	CNS006ON	AL065629 Drosophila
8	48	0.5	922	12	CNS0073W	AL066784 Drosophila
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ALIGNMENTS

CNS0091P 925 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL053013
AL053013.1 GI:4934461

GSS.

KEYWORDS

SOURCE

ORGANISM

fruit fly.

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

Genoscope.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 925)

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqreffgenoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> the BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

PI and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

1. .925

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

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[illegible]


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SOURCE EST.
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          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 452)
AUTHORS Sasaki, T. and Yamamoto, K.
TITLE Rice cDNA from panicle (2000)
JOURNAL Unpublished (2000)
COMMENT Contact: Takuji Sasaki
          National Institute of Agrobiological Resources
          Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
          305-8602, Japan
          Tel: 81-298-38-7441
          Fax: 81-298-38-7468
          Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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ACCESSION AU069689
VERSION AU069689.1 GI:5005072
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          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 615)
AUTHORS Yamamoto, K. and Sasaki, T.
TITLE Rice cDNA from callus (1998)
JOURNAL Unpublished (1998)

```

```

COMMENT Contact: Takuji Sasaki
          National Institute of Agrobiological Resources
          Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
          305-8602, Japan
          Tel: 81-298-38-7441
          Fax: 81-298-38-7468
          Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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QY 2641 TGAGCGCAGGGGGTGGAGCG 2661
Db 74 GGGACGACGCGACCGCGAAGC 54

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DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
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ACCESSION AL053013
VERSION AL053013.1 GI:4934461
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
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REFERENCE 1 (bases 1 to 925)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
          - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
          collaboration with the Berkeley Drosophila Genome Project (BDGP).
          The BDGP is constructing a physical map of the Drosophila
          melanogaster genome using these BACs. For further information
          please see http://www.fruitfly.org The BDGP Drosophila
          melanogaster BAC library was prepared by Kazutoyo Osoegawa and
          Aaron Mammosser in Pieter de Jong's laboratory in the Department of
          Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
          NY. The library is named RPCI-98 and was constructed by partial
          EcoRI digestion of Drosophila DNA provided by the BDGP from the

```

isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers
1. 925
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCi-98"
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BASE COUNT 120 a 61 c 172 t 511 others
ORIGIN

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Best Local Similarity 13.1%; Pred. No. 4; Indels 0; Gaps 0;
Matches 43; Conservative 150; Mismatches 134;

Qy 2567 CGAGGTGACACTTCGGTGTGGGTGGTGGCCAGCGTGGTGGGCGCATAGC 2626

Db 891 SSSBSSSTSSMSSSSSSSSSSSGTSSACVKCNASSSCCGCGMACCMCSSS 832

Qy 2627 GCTCCTGAGCTCAATGACGCGAGGGGTGAAGCACAAAGCCGTGATCTATAGACGTG 2686

Db 831 SCCGSASARGVKRASGAGRGGGGSGASASHSSSSACBSSSSSCSASCSASSSSAS 772

Qy 2687 GTGTAAAGGTACAGAGCTGTGCCAGAGGGTGGTGGCGGAGCCCTCGGGAGGGCG 2746

Db 771 SRSRSGGAGGSSSSSSSSSSSAGSVSSSSSSSSSSSVSSVSSVSSMSSCS 712

Qy 2747 TCCTACCAAGCTCTGAGCTTCGGCTGTGCTGTGCTCATACATCTGCGCGGATGCTGT 2806

Db 711 BSSSASASSSSSSSSSASCSCCTSWSCSTASMSAARSSSSSSSSSSMSAS 652

Qy 2807 GATGATGCTGTGTGGCTTGGTCTCTCTTCTCGGCTGTTCGACGACATGCGCTGGC 2866

Db 651 SSASSSSASSSSSSSGSSSAGBSMSGGSGSVSSAGSMSSSVSSSGRSSGGG 592

Qy 2867 CCTGGAGAGCTCTGCTCTCCGCC 2893

Db 591 GGVGGSSSSSGSGSGSGSVCS 565

RESULT 12

CNS00JRF/c

LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC:
DEFINITION BACR39E22 of RPCi-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL076642.1 GI:4956190

VERSION

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (02-JUN-1999) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCi-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCi-98"
/clone="BACR39E22"
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Best Local Similarity 36.8%; Pred. No. 4.8; Indels 0; Gaps 0;
Matches 127; Conservative 44; Mismatches 174;

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Qy 8923 GCCTCGGCTTCCCTCCCGGAGATTGCTGATATCCCGGGGTTCCCTTCCGCC 8982

Db 977 TKSTGCCCTTCSCCGSCCTCCSCCGGGGCGGCGCCCKGTSCCGCGSCGG 918

Qy 8983 CCTATATGGGGTTCATCAATTGATTTACAAAGCAGAGGAGTCGTGGCGGTG 9042

Db 917 GCTTKCGGSGGTGKBTGTTCGGGCGSCGSKGSGCTCGCGCKGCGCTCTTGTG 858

Qy 9043 TGGGTTCTTAGCCTGCTCATCTGCTAGCCCTCTTCGGGTGAACATACTCTGCG 9102

Db 857 CGTGTTGGTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 798

Qy 9103 GCAAGTCCGGTACATCATCTGCTGAGGAGTTCCTCCCGCTCCCGCCAGGCTC 9162

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Qy 9163 TCCCGCTGGGTAAAGGCGCGCTTGGAGGCGATGCTGCTGCTGCTGCTGCTG 9207

Db 737 GKGCGTCTGCTCTTTCGCGCGCGGCTGGGTGSSGCGTGTGTT 693

RESULT 13

BI329221/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota;

Mammalia;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: rcs@nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM1136 row: e column: 03

High quality sequence start: 45

High quality sequence stop: 639.


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/note="end : T7"

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Best Local Similarity 19.0%; Pred. No. 9.7;
Matches 48; Conservative 111; Mismatches 93; Indels 0; Gaps 0;

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Db 603 CAGSSWGGGAVSGSGSGGCGGVSASSCSAGGSCSKCCGSGGTSGGGSGGGCG 662

QY 723 TGCACCGACGTTGTGGCCACTGTATCAGCGGGTTTGGCTGCGGCTGGCAAGTCC 782
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Db 663 MGSGCCGSGWBGTSSSGBSWCGSSASCACVSSBSKYSKSGTWSGYSSGSGSGGA 722

QY 783 GCGGCCCCAGCTGTTGGGAACTGGGACCTGTACGGCCCTTGTGGCTCTCGGCTTAC 842
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QY 843 GTAGCCGGGATCCTGGGTCTGGCGGAGGTTTACTCCGGGCTCTGACAGTTGGTTGCG 902
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Db 783 TTTBTBSSBYSSBBBBSSTSTBTSBSSSSSTSBTTBSBSETTTTBTBTTBBB 842

QY 903 TTGAGGCGCCGG 914
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Db 843 BTTSTSTSSSS 854
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Job time : 6430 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2002, 00:04:45 ; Search time 156 seconds
(without alignments)
14793.120 Million cell updates/sec

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Perfect score: 9395

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
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- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7979	84.9	9392	1	US-08-466-033-14
2	7979	84.9	9392	1	US-08-444-733-14
3	7979	84.9	9392	2	US-08-464-134-14
4	7979	84.9	9392	2	US-08-461-361-14
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21	7106.6	75.6	9122	2	US-08-417-629B-1
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23	2141.8	22.8	2561	1	US-08-638-911A-26
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25	2140.2	22.8	2561	1	US-08-638-911A-28
26	2084	22.2	2388	1	US-08-638-911A-56
27	2005.2	21.3	2379	1	US-08-638-911A-52

28 1883.8 20.1 2232 1 US-08-638-911A-53 Sequence 53, Appl
29 1674.2 17.8 1967 1 US-08-638-911A-51 Sequence 51, Appl
30 1568.6 16.7 1848 1 US-08-638-911A-34 Sequence 34, Appl
31 1351.2 14.4 1548 1 US-08-638-911A-40 Sequence 40, Appl
32 1315 14.0 9493 2 US-08-639-857-23 Sequence 23, Appl
33 1184 12.6 1377 1 US-08-638-911A-38 Sequence 38, Appl
34 1110.8 11.8 1290 1 US-08-638-911A-55 Sequence 55, Appl
35 1080 11.5 1288 1 US-08-466-033-39 Sequence 39, Appl
36 1080 11.5 1288 1 US-08-444-733-39 Sequence 39, Appl
37 1080 11.5 1288 2 US-08-464-134-39 Sequence 39, Appl
38 1080 11.5 1288 2 US-08-461-361-39 Sequence 39, Appl
39 1080 11.5 1288 2 US-08-485-910-39 Sequence 98, Appl
40 981 10.4 1181 1 US-08-466-033-98 Sequence 98, Appl
41 981 10.4 1181 1 US-08-444-733-98 Sequence 98, Appl
42 981 10.4 1181 2 US-08-464-134-98 Sequence 98, Appl
43 981 10.4 1181 2 US-08-461-361-98 Sequence 98, Appl
44 981 10.4 1181 2 US-08-485-910-98 Sequence 98, Appl
45 936.6 10.0 1302 3 US-08-932-823A-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-466-033-14
; Sequence 14, Application US/08466033
; Patent No. 5766840
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Wages, John
; APPLICANT: Young, Lavonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466.033
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/389,886
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,509
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,729
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,271
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,558
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,543
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,985
; FILING DATE: 20-MAY-1994

ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 9392 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HGV-PNF 2161 Variant
FEATURE:
NAME/KEY: CDS
LOCATION: 459..9077
US-08-466-033-14

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DB	121	GTGATGACAGGGTTGGTAGTGTGAATCCCGGTCAATCTGGTAGCCACTATAGTGGGT	180
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DB	241	GTTGGCCCTACCGGTGTGAATAAGGGCCCGACGTCAGGCTCGTGTAAACCGAGCCCGT	300
QY	303	CACCCACTGGGCAACGACGCGCACGTACGGTCCAGTCCGCTTCAATGTCTCTCTTG	362
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QY	363	ACCAATAGGTTTATCCGGCGAGTTGACAAGGACACAGTGGGGCGGGGTTATGGGAAG	422
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QY	423	GACCCCAACCCCTGCCCTTCCCGGTGGCGCGGAAATGCAATGGGGCCACCGCTCCGCG	482
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QY	483	CGGCGCTGCAGCGGGGTAGCCCAAGAAATCCTTCGGGTGAGGGGGGTGCGATTTCTTT	542
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QY	543	TTCTATACCATCAGGAGTCTCTCTGCTCTCTGCTGCTGAGCGCGGGGCAATTCG	602
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QY	603	GCCCGCGCCACCGCTTGTGAGCGGAATGGCAATATTTCTCACAATTTGCTGTGCC	662
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DB			
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DB	720	TGCACCTGACCAATGCTGGCCACTGTATCAGGGGGGTTTGGCTGTGGCGCTGGCAAGTCC	779
QY	783	GGGGCCAGCTCGTTGGGGAACCTGGGAGCCCTGTAGGGCCCTTGTGGTCTCGGGCTTAC	842
DB	780	GGGGCCAACTGCTGGGGAGCTGGGTAGCCCTATACGGGCCCTGCGGTCTCGGCCTAT	839
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DB	840	GTGGCTGGGATCCTGGGCTGGGTGAGGTGTTCTCGGGTGTCTTAACGGTGGGAGTCGG	899
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DB	900	TTGACGCGCGGGCTTACCCGGTGCCTAACCTGACGTGTGCAGTCCGCTGTGAGCTAAG	959
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DB	1200	TACGGGTTGACTTTGGCAGACCTGCTCTGCAGGGCCACGGTTTCGGCTTTTCGAGTGG	1259
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QY	1623	CTGACCGCTCGGCTCTTTCATGTGGCACTGTGTGGGAGTGTGTGGCCGAAACCGGG	1682
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DB 1800 GGGAGAGCAACCCGGTGGGTCGCCCTGGGTTTGGGTCCTACACCATGACCAAGATC 1859
QY 1863 CGGGATTCCTCGCATTTGGTGAATGTCCACACAGGACATAGAGCCCTCCGACTGGAACG 1922
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QY 1923 TTCGGGTTCCTCCCGGAGTCCCGCCCAATTAACAATGATGCCCTAGGCAAGGATG 1982
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QY 1983 TCTGAGGCAATGGGCGGAGCTGGGCTTACGGGGGGTCTACAGGCCCTGCTGGTTCGACAG 2042
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DB 2040 TGTTCGAAGCTGATGGGAAGCGAAATCCGGTTTCCCGGGGTTCGATGGCTCTCTTCG 2099
QY 2103 GGTAGACCTGACGGTTTATACACATCCAGGGGACCTGCGAGGAGTGGATCGGGGCAAC 2162
DB 2100 GGCAGGCCCTGATGGGTTTATACATCCAGGGTCACTTTCAGGAGGTGGATCGAGGCAAC 2159
QY 2163 TTTATCCCTCCCTCCACGCTGGTGTCTTGGATTTTGTATTTGTCTGCTCTATCTGATG 2222
DB 2160 TTTATCCCGCCCGCGCTGGTGTCTTGGACTTTGTATTTGTCTGCTGTTATACCTGATG 2219
QY 2223 AAGCTGGCTGAGGCAACGGTTGGTCCCGTTGATCTTCTGCTGCTGCTGGTGGTGAAC 2282
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DB 2280 CAGCTGGGAGTCTTAGGCTGGCGCTGTGGAAGCGCGGTGGCAGGTGAGTCTTCGCG 2339
QY 2343 GGCCCTGCTGCTATGTTGGTGGGCTTCCCACTGTCAGTATGATAGTCTAGCA 2402
DB 2340 GGCCCTGCTGCTGCTGGTGTGGGACTCCCGGCTGCTAGTATGATTTGGGTTGGCA 2399
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DB 2400 AACCTGGGTTGATCTTGGAGTGGGAGTGGGAGCCCAACGCTGATGTTCTGCTGTTGG 2459
QY 2463 AAGCTGCTCGGGAGCTTCCCGCTGGACCTTTTGTATGGGATTTCCGCGACCGCGGG 2522
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DB 2640 ACGCAGGGGGTGGAGCACAGCCGCTGATCTATAGGACGTGGTGAAGGGTACCAG 2699
QY 2703 GCTGTCCGCGAGAGGTGGTGGGAGCCCGCTCGGGAGGGGCGCTCTACCAAGCTTCTG 2762
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DB 2760 ACGTTGCGCTGGTGGTGGCTTCGATCTGGCCAGATGCTGTGATGATGCTGGTGGT 2819
QY 2823 GCTTTGGTCTCTCTTGGCCCTGTTCGAGGCACTGGAGTGGGCCCTGGAGGAGTCTCTG 2882
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DB 3240 GTTGTATCCGAGGCTGCGGAAAGGCTTCTTGGGGTCAACAAAGGCTGCTTTCAGCT 3299
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QY 9003 CAATTGGATTTCACAGCCAGAGAGTCTGCTGCGGTGGTTCCTTAGCCCTGCTC 9062
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Db 9360 GGTAAAGCTCGGCCAAAGCGCGGTCTTACT 9392

RESULT 2

US-08-444-733-14
; Sequence 14, Application US/08444733
; Patent No. 5824507
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Wages, John
; APPLICANT: Young, LaVonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; Cloning Thereof
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,733
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/389,886
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,509
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,729
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,271
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,558
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,543
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,985
; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9392 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HGV-PNF 2161 Variant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 459..9077
US-08-444-733-14

Query Match

84.9%; Score 7979; DB 1; Length 9392;

Best Local Similarity 90.7%; Pred. No. 0;			
Matches 8515; Conservative 1; Mismatches 876; Indels 1; Gaps 1;			
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QY	123	GTGGTGACAGGGTTGGTAGGTGCTTAATCCCGGTGATCCTGCTAGTGGGTGGGT	182
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QY	243	GCTGCCCTACCGGTGTAATGAAGGCCCGGACGTCAGGCTCGCTGTTAAACCGAGCCCGT	302
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QY	423	GACCCAAACCTGCTCCCTGCGGTGGCGGGAATGATGGGCGACCCAGCTCCCGG	482
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QY	903	TTGAGCGCGGGTCTACTGATGCCAACCTGAAGTGTGAGTGAATGTGACGCTTAAG	962
Db	900	TTGAGCGCGGGTCTACTCGGGTGTACCTTACCTGAGCTGTGAGTGGCTTAAG	959
QY	963	TGGGAAGTGTGTTGGAGATGAGTGTGAGGAGTGGGCTCCCAATTTACTGGATTTGAA	1022
Db	960	TGGGAAGTGTGTTGGAGATGAGTGTGAGGAGTGGGCTCCCAATTTACTGGATTTGAA	1019
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QY	1203	TACGGTTGAAGTGGCAGTCATGCTCTGAGGGCTTAAGGGTGGGTATTCCTACTGG	1262
Db	1200	TACGGTTGAAGTGGCAGACCTGCTCTTGCAGGGCAACGGTTCGGTTTTTTCAGTGG	1259
QY	1263	GAGAGGCTGCGGATCGAGGGAATGTCAGCTCTTGTGTGACTGCCCAACGCCCTCG	1322
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Db	1740	GCTGTGCCCTTCGTCAACAGGACAACTCCCTTACCATTAAGGGGCCCTCGGCAACAG	1799
QY	1803	GGGAGAGCAACCGGTGGGTGGGCTGGGCTTTGGGTTTGGGCTTACACCATGACCAAGATC	1862
Db	1800	GGCCAGGCAACCGGTGGGTGGGCTGGGCTTTGGGTTTGGGCTTACACCATGACCAAGATC	1859
QY	1863	CGGGATTCCTCATTTGGTGAATGTCACACACAGCCATAGAGCCTCCGACTGGAAC	1922
Db	1860	CGAGATACCTACATCTGGTGGAGTGTCCACACACAGCCATTTGAGGCTCCACCGGAGC	1919
QY	1923	TTTCGGTCTTCCCGGAGTCCCGGCCATTAACAACTGCATGCCGTAGGCACGGAAGTG	1982
Db	1920	TTTCGGTCTTCCCGGAGTCCCGGCCCTCTCAAACTGCATGCTCTTGGGACGGAAGTG	1979
QY	1983	TCGAGGCAATGGGCGGAGTGGGCTTACGGGGGGTCTACGAGGCTCTGTTGCGAGG	2042
Db	1980	TCGAGGCAATGGGCGGAGTGGGCTTACGGGGGGTCTACGAGGCTCTGTTGCGAGG	2039
QY	2043	TTTCGGAGCTGATGGGACCGGAATTCGGTTTGGCCGGGTACGCATGGCTGCTCT	2102
Db	2040	TTTCGAGCTGATGGGAAGCGGAATTCGGTTTGGCCGGGTTCGATGGCTCTCTCG	2099
QY	2103	GATAGACCTGACGGTTTCATACAGTCCAGGGCCACTCGAGGAGGTGATCGGGCAAC	2162
Db	2100	GGCAGGCTGATGGGTTTATACATGTCAGGGTCACTTCAGGAGGTGATGAGGCAAC	2159

Qy	2163	TTCA	TCCCTCC	TCCACG	CTGGT	TGCTCT	TGGATT	TGTG	TTGTTG	CTCTG	CTCTAT	CTGATG	2222
Db	2160	TTTT	TTTT	TTTT	TTTT	TTTT	TTTT	TTTT	TTTT	TTTT	TTTT	TTTT	
Qy	2223	AAGC	TGGCTAG	GACG	AGTTGG	TCCCGG	TGATCT	TGCTTC	TGCTGCT	GTGGTGG	TGGTGAAC	2282	
Db	2220	AAGC	TGGCTAG	GACG	AGTTGG	TCCCGG	TGATCT	TGCTTC	TGCTGCT	GTGGTGG	TGGTGAAC	2279	
Qy	2283	CAGT	TGGCGG	TTCTAG	AGCTGC	CGGCTG	TGAG	CGCTGC	CGTGGG	TGAGT	TTTTCG	2342	
Db	2280	CAGC	TGGCACT	CTAG	GGCTG	CGGCTG	TGAG	CGCGCG	CTGG	CAGT	TGAGTCTTC	2339	
Qy	2343	GGCC	TGCTTC	ATG	TGGT	TTTGG	GCCTTCC	ACTG	TCAGT	ATGAT	CTAGGCTTAG	2402	
Db	2340	GGCC	TGCTTC	ATG	TGGT	TTTGG	GCCTTCC	ACTG	TCAGT	ATGAT	CTAGGCTTAG	2399	
Qy	2403	AAC	TGGT	TTG	TACT	TTTC	GGTGG	AGCC	CTC	AGC	CCCTCAT	2462	
Db	2400	AAC	TGGT	TTG	TACT	TTT	AGAT	TTGG	AGCC	CTC	AGT	2459	
Qy	2463	AAGC	TCGCTCG	GGAG	CTTCC	CGCTGG	CAC	TTT	TGAT	GGGAT	TTTCGG	2522	
Db	2460	AAGC	TCGCTCG	GGAG	CTTCC	CGCTGG	CAC	TTT	TGAT	GGGAT	TTTCGG	2519	
Qy	2523	CGAC	CTCTG	CTCG	GGGCG	AGTTCT	CTG	ATCG	ATCAT	TCG	AGGTGG	2582	
Db	2520	CGAC	CTCTG	CTCG	GGGCG	AGTTCT	CTG	ATCG	ATCAT	TCG	AGGTGG	2579	
Qy	2583	GTGT	TGGGCT	TGGT	TGG	CGCAG	CTGTG	TGG	CCAT	TAG	CGCTC	2642	
Db	2580	GTGT	TGGGCT	TGGT	TGG	CGCAG	CTGTG	TGG	CCAT	TAG	CGCTC	2639	
Qy	2643	AGC	CAGGGG	GTGA	AGC	ACAGG	CGGTG	AT	AG	ACG	TGTTAA	2702	
Db	2640	AGC	CAGGGG	GTGA	AGC	ACAGG	CGGTG	AT	AG	ACG	TGTTAA	2699	
Qy	2703	GCT	TGCGC	CAG	AGGTGG	TGCG	GAG	CCCTC	TCG	GGGAG	GGCGCT	2762	
Db	2700	GCA	TCCGTC	CA	AAAGG	TGGT	TGAG	AG	CCCTC	TCG	GGGAG	2759	
Qy	2763	ACGT	TTCCGCT	TGGT	TGG	CCCTCAT	AT	CTCG	CCG	ATGCT	GTATG	2822	
Db	2760	ACCT	TTCCGCT	TGGT	TGG	CCCTCGT	ACA	TC	TG	CCAG	ATGCT	2819	
Qy	2823	GCCT	TGCTCT	CTCT	TCG	SCCTG	TTTC	GAC	GAC	TCG	GA	2882	
Db	2820	GCCT	TGCTCT	CTCT	TCG	SCCTG	TTTC	GAC	GCTT	GG	GA	2879	
Qy	2883	GTCT	CCCGG	CCCTCG	TAC	GGG	AGCTTGG	CAC	GGGTGG	TGAGT	GCTGT	2942	
Db	2880	GTGT	CCCGG	CCCTCG	TAC	GGG	AGCTTGG	CAC	GGGTGG	TGAGT	GCTGT	2939	
Qy	2943	GAGA	AGGCC	ACC	ACCA	TCG	AGT	CTC	CA	AGAT	GTGCG	3002	
Db	2940	GAGA	AGGCC	ACC	ACCA	TCG	AGT	CTC	CA	AGAT	GTGCG	2999	
Qy	3003	GACC	AGTGG	GGCTTT	CTCG	CGCG	CTG	TC	AG	GAG	CCCTT	3062	
Db	3000	GAT	CAT	TGG	GGCTTT	CTCG	CGCG	CTG	TC	AG	GAG	3059	
Qy	3063	TTGG	AGCC	TTG	TCA	TCT	ACT	AGG	AGG	ACTG	TCGC	3122	
Db	3060	CTT	GA	CCCTG	TCA	TCT	ACT	AGG	AGG	ACTG	TCGC	3119	
Qy	3123	CTGT	CTCG	GAC	AGT	CCGCT	TCAT	TGG	TTT	TAC	CCGTGG	3182	
Db	3120	TTGT	CTCG	GAC	AGT	CCGCT	TCAT	TGG	TTT	TAC	CCGTGG	3179	
Qy	3183	CTCA	TGCG	GCTCT	TTCC	AGG	ATG	GA	ATCA	TTT	GCCTCC	3242	
Db	3180	CTCA	TGCG	GCTCT	TTCC	AGG	ATG	GA	ATCA	TTT	GCCTCC	3239	

QY	3243	GTTCATCTCGTCGGTGGGAAAGGCGCTTCCTGGGGGTACGAAGGCAGCCTTGACAGGT	3303
DB	3240	GTTCATCTCGGACGGTCGCGAAAGGCGCTTCCTGGGGGTACAAAGGCTGCCTTGACAGGT	3299
QY	3303	AGGATCCTGACTTACATCCAGGAAAGCTCATGGTGTGTGGGACGGCTACGCTCACAAGC	3362
DB	3300	CGGATCCTGACTTACATCCAGGAAAGCTCATGGTGTGTGGGACGGCTACGCTCCGAAGC	3359
QY	3363	ATGGGCACATGCTCTGAATCGCCTGCTGTTCACAACCTTTCATGGGGCTTCATCCGGAACC	3422
DB	3360	ATGGGAACATGCTTGAACGCGCTGCTTTCACGACCTTCCATGGGGCTTCATCCGGAACC	3419
QY	3423	ATCGCCACGCGCGTGGGGGCCCTTAATCCAGGTGGTGTGTCAGCCAGTGATGAGTCAAG	3482
DB	3420	ATCGCCACACCGCTGGGGGCCCTTAATCCAGATGGTGTGTCAGCCAGTGATGATGTCAAG	3479
QY	3483	GTGTACCCGCTTCCAGATGGGCAACTCTGTGTGACGCCCTGCACCTTGCAGCGGAGTCC	3542
DB	3480	GTGTATCCACTCCCGATGGGGCTACTCTGTTAAACACTGTGTACTTGCAGCGTGTAGTCC	3539
QY	3543	TGTTGGGTATTAGATCCGACGGGGCTTTGTGCCATAGGCTTGAGCAAGGGGACAAAGGTT	3602
DB	3540	TGTTGGGTATCATGATCCGACGGGCCCTATGCCATGGCTTGAGCAAGGGGACAAAGTG	3599
QY	3603	GAGCTGGATGTGGCCATGAGAGTCTCTGACTTCCGTGGTGTCTGTGGTTCACCGTCTCT	3662
DB	3600	GAGCTGGATGTGGCCATGAGAGTCTCTGACTTCCGTGGTGTCTGTGGTTCACCGTCTCTA	3659
QY	3663	TGCGACAAGGGCACGCAGTAAGAACTCTGCTGACTGCTCCACTCTGCGCGGACAGGTT	3722
DB	3660	TGTGACGAAGGGCACGCAGTAGGAATGCTGTGCTGTCTGCTGCTACTCCGGTGTGAGGTC	3719
QY	3723	ACTGCGCGCGATTACTATGCGCGTGGACTCAAGTACCACAAGATGCCAAGACTACCACA	3782
DB	3720	ACCGCGCACGGTTCACTATGCGCGTGGACCCAGTGCACAAGATGCCAACCACACTACT	3779
QY	3783	GAACCCCTCTCGGTGCGCGCAAAAGGAGTTTCAAGAGGCCCCGTGTGTTATGCTCTACG	3842
DB	3780	GAACCCCTCTCGGTGCGCGCAAAAGGAGTTTCAAGAGGCCCCGTGTGTTATGCTCTACG	3839
QY	3843	GGGCGGGAAGACGCCCGGTACCGTGTGGATGACGGCAACATGCGCCACAAGGCTCTG	3902
DB	3840	GGAGCGGGAAGACGACTCGCTGCCGTGTGGATGACGATAACATGGGCAACAGGCTCTTA	3899
QY	3903	ATCTTGAACCCGTGCGTAGCTACCGTAGGGCCCATGGGCCCATATGATGGCGGTGGCG	3962
DB	3900	ATCTTGAACCCCTCAGTGGCCACTGTGCGGCCATGGGCCGTACATGAGCGGCTGGCG	3959
QY	3963	GGGAACACCCCAAGTATTTACTGTGGCCATGACACCACTGTCTTCAAGAATCACTGAC	4022
DB	3960	GGTAACATCCAAGTATATCTGTGGCATGATACAACCTGCTTTCACAAGATCACTGAC	4019
QY	4023	TGCGCCCTTACGTATTCACCTTACGGAAGTTTTTGGGCCAACCCCTTAGGCAGATGCTGAG	4082
DB	4020	TCCGCCCTTGAGTATTCACCTATGGAGGTTTTTGGGCCAACCCCTTAGGCAGATGCTACGG	4079
QY	4083	GGTGTGTGCGTGGTCATTTCTGACGAGTGCCACAGTCATGACTCAACTGTGTGTGGGC	4142
DB	4080	GCGGTTTCTGGTGGTCATTTGTGATGAGTGCCACAGTCATGACTCAACCGTGTGTGAGC	4139
QY	4143	ATTGGGCGTGTGAGGAGCTGGCGCGGAGGATGTGGAGTGCAATGGTGCTCTACGCCACT	4202
DB	4140	ATTGGGAGTGTCCGGAGCTGGCGCGTGGTGGGGGTGCACTAGTGTCTACGCCACC	4199
QY	4203	GCCACCCCTCCGGATCCCAGATGACCCAGCACCCCAATCAATGATGAGACAAAACGTGAC	4262
DB	4200	GCTACACCTCCGGATCCCTTATGACGACGACACCCCTTCCATTAATTGACACAAAATTGGAC	4259
QY	4263	GTGGAGAGATCCCTTCTATGGGCATGCGATACCTCTGTAGCGGATCGGACCGGAGG	4322
DB	4260	GTGGCGGAGATTCCCTTTTATGGCATGGAATACCCCTCGAGCGGATGCGAACCGGAAG	4319
QY	4323	CATCTGCTATTCTGCCACTCCAAAGGCTGAGTGTGACGCGCTGGCGGGCGAGTTTTTCGGCT	4382

Db 8700 CTGGACAACTGCTAAACATCATCGTGGCCCTCCACGGACACGAGCGTTGAGGGTTACC 8759
QY 8763 GCAGACACAACTAAGACAAAATGAGGCTGGCAAGGTGCTGAGCGACCTCAAGCTCCCT 8822
Db 8760 GCAGACACAACTAAGACAAAATGAGGCTGGCAAGGTGCTGAGCGACCTCAAGCTCCCT 8819
QY 8823 GGCTAGCAGTGCACCGGAAGAGCGGGCATTCGGAACGCTATGCTCCGGTGGCGC 8882
Db 8820 GCGTTAGCAGTGCACCGGAAGAGCGGGCATTCGGAACGCTATGCTCCGGTGGCGC 8879
QY 8883 GGTGGGCTGAGTGGCTAGGGGGCTGTTGTGGCGCTCCAGGCTGCGGCTCCCGCTCGG 8942
Db 8880 GGTGGGCTGAGTGGCTAGGGGGCTGTTGTGGCATCCAGGCTACGGCTTCTCCCGCT 8939
QY 8943 GAGATTGCTGGTATCCCCGGGGGTTCCCGCTTCCCGCCCTATATGGGGTGGTTGAT 9002
Db 8940 GAGATTGCTGGTATCCCCGGGGGTTCCCGCTTCTCCCGCCCTATATGGGGTGGTACAT 8999
QY 9003 CAATTGGATTTCACAAGCCAGAGGAGTGCCTGGCGGTGTTGGGGTCTTAGCCCTGCTC 9062
Db 9000 CAATTGGATTTCACAAGCCAGAGGAGTGCCTGGCGGTGTTGGGGTCTTAGCCCTGCTC 9059
QY 9063 ATCTAGACCTCTTCGGGTGAACAAATTCATCTGTTGGCGCAAGTCCGCTGACTGATC 9122
Db 9060 ATCTAGACCTCTTCGGGTGAACAAATTCATCTGTTGGCGCAAGTCTGCTGACTGATC 9119
QY 9123 ATCACTGGAGGAGTTCGCCCGCTCCCGCCCGCCAGGGGTCTCCCGCTGGTAAAAAGG 9182
Db 9120 ATCACTGGAGGAGTTCGCCCGCTCCCGCCCGCCAGGGGTCTCCCGCTGGTAAAAAGG 9179
QY 9183 CCGGCTTTGGGAGGATCGTGGTACTAAACCCCTGGCAGGCTCAAGCCCTGATGGTC 9242
Db 9180 CCGGCTTTGGGAGGATCGTGGTACTAAACCCCTGGCAGGCTCAAGCCCTGATGGTC 9239
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Db 9240 TAATGACACTGCCACTTCGCTGGGCTGCTACCTTATAGCGTAATTCGCTGACTAGGCG 9299
QY 9303 TGCTGCAGACGCTCCCGGATGGGACAGTGCATGCTGATCTGAAGGGTGCACCC 9362
Db 9300 TGCTGCAGACGCTCCCGGATGGGACAGTGCATGCTGATCTGAAGGGTGCACCC 9359
QY 9363 GGTAGAGCTCGGCCCAAGCGGGTCTACT 9395
Db 9360 GGTAGAGCTCGGCCCAAGCGGGTCTACT 9392

RESULT 3
US-08-464-134-14
; Sequence 14, Application US/08464134
; Patent No. 5849532
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Wang, John
; APPLICANT: Young, LaVonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,134
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/389,886
; FILING DATE: 15-FEB-1995
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; APPLICATION NUMBER: US 08/357,509
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,729
; FILING DATE: 26-OCT-1994
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; APPLICATION NUMBER: US 08/344,271
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,558
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,543
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,985
; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
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; TELEPHONE: (415) 324-0880
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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9392 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HGV-PNF 2161 Variant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 459..9077
; US-08-464-134-14

Query Match 84.9%; Score 7979; DB 2; Length 9392;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 8515; Conservative 1; Mismatches 876; Indels 1; Gaps 1;
QY 3 ACGTGGGGGGTTGATCCCGCCCCCGGCGACTGGGTGCAAGCCCATAAACCGAGCGCT 62
Db 1 ACGTGGGGGGTTGATCCCGCCCCCGGCGACTGGGTGCAAGCCCATAAACCGAGCGCT 60
QY 63 ATCTAGTAGACGAATGACTCGGCGCGACTCGGCGCGCCCAAGGCTGTGATGCG 122
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QY 123 GTGGTGACAGGGTTGGTAGGTGCTAAATCCCGGTCTATCTGTAGCCACTATAGTGGGT 182
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QY 183 CTTAAGAGAAGTCAAGACTCTCTTGTGCGCTGCGGCGAGACCGCGCAGGTCACAGGT 242
Db 181 CTTAAGAGAAGTCAAGACTCTCTTGTGCGCTGCGGCGAGACCGCGCAGGTCACAGGT 240
QY 243 GCTGGCCCTACCGTCTGATAGGCGCGCGAGTCAAGGCTCGCTGTTAAACCGAGCGCT 302
Db 241 GTTGGCCCTACCGTGGGAATAAGGCGCGCGAGTCAAGGCTCGCTGTTAAACCGAGCGCT 300
QY 303 CACCCACCTGGGCAACGACGACGCGCCACGTCAGGTCACGCTCGCCCTTCAATGCTCTCTTG 362

Db	301		TACCCACCTGGGCAACAGACGCCACGTTACGGTGCACGTGCGCCCTCAATGTCCTCTTG	360
Qy	363	ACCAATAGGTTTATCCGGCGAGTTGACAAGACCACTAGTGGGGCCGGGGTTATGGGAAG	422	
Db	361	ACCAATAGGCGTAGCGCGGAGTTGACAAGACCACTAGTGGGGCCGGGGCT-TGAGAGG	419	
Qy	423	GACCCAAACCCCTGCCCTTCCCGGTGGGCGGGAAATGCATGGGGCCACCCAGCTCCGCG	482	
Db	420	GACTCCAAGTCCCGCCTTCCCGTGGCGGGAAATGCATGGGGCCACCCAGCTCCGCG	479	
Qy	483	CGGCCTGCAGCGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGTGCGATTTCCTTT	542	
Db	480	CGGCCTGCAGCGGGTAGCCCAAGAATCCTTCGGGTGAGGGCGGGTGCGATTTCCTTT	539	
Qy	543	TTCTATACCATATGTCAGTCCCTTCCTGCTTCCTGCTTGTAGGGCGGGCCATTCTG	602	
Db	540	TTCTATACCATATGCGAGTCCCTTCCTGCTTCCTGCTTGTAGGGCGGGCCATTCTG	599	
Qy	603	GCCCGGCCACCCACGCTTGTGAGCGAATGGCGAATATTTCTCACAAATGCTGTGCC	662	
Db	600	GCCCGGCCACCCACGCTTGTGAGCGAATGGCGAATATTTCTCACAAATGCTGTGCC	659	
Qy	663	CGGAAGACATCGGTTCTGCCGGAAGCGGATGCTTGTGTGGCCCTGGGGTGACGGTT	722	
Db	660	CGGAGGACATCGGTTCTGCCGGAAGCGGATGCTTGTGTGGCCCTGGGGTGACGATT	719	
Qy	723	TGCACCGACCGTTGCTGGCCACTGATACGCGGCTTGGGCTGTGCGCCTGGCAAGTCC	782	
Db	720	TGCACTGACCAATGCTTGGCCACTGATACGCGGCTTGGGCTGTGCGCCTGGCAAGTCC	779	
Qy	783	CGCGCCAGCTCGTTGGGAACCTGGGGAGCCGTACGGGCCCTTGTGCGTCTCGGCTTAC	842	
Db	780	CGCGCCACTGTTGGGGAGCTGGTACGCTATACGGGCCCTGTGCGTCTCGGCTAT	839	
Qy	843	GTAGCCGGATCTCGGTTGTGGCGAGGTTTACTCCGGGGTCTTGACAGTTGTGTGCG	902	
Db	840	GTGGCTGGGATCTGGGCCCTGGGTAGGTGTACTCGGGTGCTTAACGGTGGGAGTCCG	899	
Qy	903	TTGAGGCGCGGCTACTCTGATGCCCAACCTGAAGTGTGCAGTAGATGTGACGTTAAG	962	
Db	900	TTGAGCGCGCGGCTACCCGGTGCCCTAACCTGACGTGTGCAGTCCGCTGAGCTAAG	959	
Qy	963	TGGGAAGTGAAGTTTGGAGTGGAGTGAAGTGGCTCCAAATTAATGGAATTTGGAA	1022	
Db	960	TGGGAAGTGAAGTTTGGAGTGGAGTGAAGTGGCTCCAACTACTGGAATTTGGAA	1019	
Qy	1023	TACCTTTGGAAGTCCCATTTGAATTTGGAGGAGGTGATGAGCCTGACCCCTCTGTG	1082	
Db	1020	TACCTCTGGAAGTCCCATTTGAATTTGGAGGAGCGTGAAGGCTGACCCCTCTGTG	1079	
Qy	1083	GTTTGGGTGCGCCATTTGCTTGTGGAGCAACGATGTCAATGTTTCCCTCTGCTGGT	1142	
Db	1080	GTTTGGGTGCGCCATTTGCTTGTGAGCAACGATGTCAATGTTTCCCTCTGCTGGT	1139	
Qy	1143	ACGATGCGGGGATGTGGAAGCGCCCGCCTCCGCTTTTGGGTCCCGCCCTTTGAC	1202	
Db	1140	ACGATGCGGGGATGTGGAAGCGCCCGCCTCCGCTTTTGGGTGACGCCCTTTGAC	1199	
Qy	1203	TACGGGTTGAAGTGGCAGTCATGCTCTGCAGGGCTAACGGGTGCGGTATTTCCACTGGG	1262	
Db	1200	TACGGGTTGACTTTGGCAGACCTGCTTTGAGGGGCAACGGTTTGGCTGACCTGGG	1259	
Qy	1263	GAGAGGTGTGGGATCGAGGATGTCAAGCTTGTGTGACTGCCCAAGGCCCTCTGG	1322	
Db	1260	GAGAAGGTGTGGGACGTGGGAACGTTACGCTTCACTGACTGCCCTAACGGCCCTGG	1319	
Qy	1323	GTTTGGGTCCCGCCCTTTTGCAAGCGGTTGGGTGGGGGACCCCATCACCATTTGAGC	1382	
Db	1320	GTGTGGTTGCCACGCTTTTGCCNAGCAATCGGCTGGGTGACCCCATCATTTTGGAGC	1379	
Qy	1383	CACGGACAAAACAGTGGCCCTTATCATGCCCCCAATATGTATGGGTGTGTCTCGCTA	1442	

Qy	2523	CGACCTCTGTGCTCGGGCCGAGTTCCTTCGATGTCACATTCGAGGTGGACACTTCG	2582
Db	2520	CGACCTCTAGTGTCTGGGGCCGAGTTCCTGCTTCGATGTCATATTCGAGGTGGACACTTCG	2579
Qy	2583	GTGTTGGGCTGGTGTGGCCAGCTGCTGGCTTGGGCCATAGCGCTCCCTGAGCTCAATG	2642
Db	2580	GTGTTGGGCTGGTGTGGCCAGTGTGGTACCTTTGGGCCATTTGGCTTCCTGAGCTCGATG	2639
Qy	2643	AGCGCAGGGGGTGAAGCACAAAGCCCTGATCTATAGGACGTGGTGTAAAGGGTACCAG	2702
Db	2640	AGCGCAGGGGGTGGAGGCACAAACCCGTGATCTATAGGACGTGGTGTAAAGGGTACCAG	2699
Qy	2703	GCTGTGCGCCAGAGGTGTGCGGAGCCGCCCTCGGGGAGGGGGCTCTCTACCAAGCTTCG	2762
Db	2700	GCAATCCGTCAAGAGTGTGAGGACGCCCTCGGGGAGGGGGCGCTGCCAAACCCCTG	2759
Qy	2763	ACGTTCCGCTGTGCTTTGGCCCTCATACATCTGGCCGATGCTGTGATGATGGTGGTGGTG	2822
Db	2760	ACCTTTGGCTGTGCTTTGGCCCTGATACATCTGGCCAGATGCTGTGATGATGGTGGTGGT	2819
Qy	2823	GCCTTGGTCTCTCTTTCGGCTGTTCGAGCGACTTGGAGCTGGGCCCTTGGAGGAGCTCTCG	2882
Db	2820	GCCTTGGTCTCTCTTTTGGCCCTGTTCGACCGCTTGGATTTGGGCTTTGGAGGAGATCTTG	2879
Qy	2883	GTCTCCCGCCCTCGTTACGGCGACTGGCAGCGGTGGTGTGAGTCTCTGTGATGCGCGGC	2942
Db	2880	GTGTCCCGCCCTCGTTTGGCGGCTTGGCTCGGGTGGTGTGAGTCTCTGTGATGCGCGGT	2939
Qy	2943	GAGAAGCCACCACTCCGACTTGGTCTCCAAGATGTGCGCAAGAGGGGCTTACCTGTGTTT	3002
Db	2940	GAGAAGCCACAAACGTCGCGCTGCTCTCCAAGATGTGTGCGAGAGAGCTTATTTGTTTC	2999
Qy	3003	GACCACATGGGCTCTTCTTCGCGCCCTGTCAAGAGAGCGCTTGTGTGAATGGGAGCGGCT	3062
Db	3000	GATCATATGGGCTCTTTTTCGCGTCTGTCAAGGAGCGCTTGTGTGAATGGGAGCGAGCT	3059
Qy	3063	TTGGAGCCCTTGTCAATCACTTAGGAGGACTGTGCGATCATCAGATGCGCGAGGAGCC	3122
Db	3060	CTTGAACTCTGTCAATCACTTAGGAGGACTGTGCGATCATACGGGATGCGCGAGGACT	3119
Qy	3123	CTGTCTCGGGCAGTGCCTCATGGGTTTACCCTGTGTAGCACGCGCGGTGTATGAGGTT	3182
Db	3120	TTGTCTCGGGCAGTGCCTCATGGGTTTACCCTGTGTGCGCCGCTGTGTGATGAGGTT	3179
Qy	3183	CTCATCGGGCTTTTCAGGATGTGAATCATTTGCTCCCGGGTTTGTCCCGACTGCACCA	3242
Db	3180	CTCATCGGGCTTTCAGGATGTGAATCATTTGCTCCCGGGTTTGTTCGCGCGCGGCT	3239
Qy	3243	GTTGTCTATCGTTCGGTTCGGAAGGCTTCTTGGGGGTTCAGAGGACAGCTTGACAGGT	3302
Db	3240	GTTGTCTATCGGAGGTTCGGAAGGCTTCTTGGGGGTTCAGAGGACAGCTTGACAGGT	3299
Qy	3303	AGGATCTCTGACTTACATCCAGGGAACGTCATGTGTTTGGGGACGGCTACGTCACGAAGC	3362
Db	3300	CGGATCTCTGACTTACATCCAGGGAACGTCATGTGTTTGGGGACGGCTACGTCGCGAAGC	3359
Qy	3363	ATGGGCACATCTGTAATGGCTGCTGTTTACAACTTTCATGGGGGCTTATCTCCGNAAC	3422
Db	3360	ATGGGAACATGCTTTGAACGGCTGCTGTTTACAGACTTTCATGGGGGCTTATCTCCGNAAC	3419
Qy	3423	ATGCCACGCCCTGGGGGCCCTTAATCCCAGGTGGTGTGAGCCAGCTGATGAGCTCACG	3482
Db	3420	ATGCCACACCCTGGGGGCCCTTAATCCCAGATGGTGTGAGCCAGCTGATGATGTACG	3479
Qy	3483	GTGTACCCGTTCCAGATGGGCAACTTCTGTTTGAAGCCCTGCATTTGCCAGGGGAGTCC	3542
Db	3480	GTGTATCCACTCCCGGATGGGCTACTTCGTTTAAACCTTGTACTTGCAGGCTGAGTCC	3539
Qy	3543	TGTTGGTATTATAGATCCACGGGGCTTTGTGCCATGCTTGACAAAGGGGACAAAGTT	3602
Db	3540	TGTTGGGTATCATAGATCCAGGGGCCCTATGCCATGCTTGAACAGGGGACAAAGTG	3599

Qy	3603	GAGCTGGATGTGGCCATGGAGGTCTCTGACTTCCGTGGTGTGGTCTGGTCTGACTACCGGTCTCTT	3662
Db	3600	GAGCTGGATGTGGCCATGGAGGTCTCTGACTTCCGTGGTGTGGTCTGGTCTGACTACCGGTCTCTT	3659
Qy	3663	TGCGACAAAGGGACGACGATAAGAAATCTGCTGTGCAGTGTCTCCACTCTCTGGCGGAGGGTT	3722
Db	3660	TGTGACGAAGGGACGACGATAGAAATGCTGTGTCTGTGCTTCACTCCGGTGGTAGGGTC	3719
Qy	3723	ACTGGCGGGGATTCACTAGGCGGTGGACTCAAGTACCAACAGATGCCAAGACTACCCACA	3782
Db	3720	ACCGGGCGGTTCACTAGGCGGTGGACCCAAAGTGCACACAGATGCCAACCACACTACT	3779
Qy	3783	GAACCCCTCCGGTGGCGGCAAAAGAGATTTTCAAGAGGCCCCGTGTTTATGCGCTACG	3842
Db	3780	GAACCCCTCCGGTGGCGGCAAAAGAGATTTTCAAGAGGCCCCGTGTTTATGCGCTACG	3839
Qy	3843	GGGGCGGAAGAGACCCCGGTACCTTGGAGTACGGCAACATGGGCCACAAAGTCTCTG	3902
Db	3840	GGAGCGGAAGAGACCTCGCTGCCCTTGGAGTACGATAACATGGGCAACAGGTCTTA	3899
Qy	3903	ATCTTGAACCCGTGGTGTAGCTACCGTAGGGCCCATGGGCCCATACATGAGCGCGCTGGCG	3962
Db	3900	ATCTTGAACCCCTAGTGGCCACTGTGCGGGCCATGGGCCGTACATGAGCGCGCTGGCG	3959
Qy	3963	GGGAACACCCCGATTTACTGTGGCCATGACACCACTGCTTTCACAAGGATCACTGAC	4022
Db	3960	GGTAACATCCAATATATCTGTGGCCATGATACAACTGCTTTCACAAGGATCACTGAC	4019
Qy	4023	TCGGCCCTTACGTATTCCACTTACGGAAGTGTTTGGCCAAACCTTACGACATGCTGAGG	4082
Db	4020	TCCCCCTGACGTATTCAACCTATGGGAGGTTTTTGGCCAAACCTTAGGCAGATGCTACGG	4079
Qy	4083	GGTGTGTCGGTGGTCAATTTGTACGAGTGCCACAGCTCATGACTCAACTGTGTGTGGGC	4142
Db	4080	GSGCTTTCGGTGGTCAATTTGTGATGAGTGCCACAGTCACTCAACCGTGTGTAGGC	4139
Qy	4143	ATTTGGGCGTGTACGGAGCTGGCGCGAGGATGTGGATGTCAAATTTGGTGTCTACGCCACT	4202
Db	4140	ATTTGGGAGTTCGGGAGCTTGGCGCGTGGGTGCGGGGTGCAACTAGTGTCTACGCCACC	4199
Qy	4203	GCCACCCCTCCGGATCCCGATGACCCAGCACCCATCAATCATTTGACACAAAATCGAC	4262
Db	4200	GCTACACTCCGGATCCCTATGACGACAGCACCTTCCATAAATTTGACACAAAATTTGAC	4259
Qy	4263	GTGGGAGAGATCCCTTCTATGGCCATGGCATACCTTCTTACGCGGATCGGACCGGAAGG	4322
Db	4260	GTGGCGGATTTCCCTTTTATGGCGATGGNATACCCCTCGAGCGGATCGGAACCGGAGG	4319
Qy	4323	CATCTCGTATTTGCGCACTCCAAGGTGAGTGGAGCGGCTTGGCGGGCGAGTTTCGGCT	4382
Db	4320	CACCTCGTGTCTGCCATTCTAAGGCTGAGTGGAGCGGCTTGTCTGGCCAGTTCTCGCT	4379
Qy	4383	AGGGGGTAATGCCATCGCCTATTACAGGGGGAAGACAGTTCTTATCATCAAGATGGA	4442
Db	4380	AGGGGGTCAATGCCATTGGCTATTATAGGGGTAAAGACAGTTCTTATCATCAAGSATGGG	4439
Qy	4443	GACCTGTGTGTGTGCTACAGACGCACTATCCACTGGGTACACTGGGAACCTTCGATTCT	4502
Db	4440	GACCTGTGTGTGTGCTACAGACGGCCTTTCACCTGGGTACACTGGGAANTTTGACTCC	4499
Qy	4503	GTCACCGATTGTGGGTAGTGGTGGAGAGGTGCTGAGGTGACCTTTGATCCCACCATT	4562
Db	4500	GTCACCGACTGTGGATTAGTGGTGGAGAGGTGCTTGTAGGTGACCTTTGATCCCACCATT	4559
Qy	4563	ACCATCTCCCTGCGCAGGTGCCCGGTGGGTGAACTGTGTGATCGACGGCGGAGGAGCG	4622
Db	4560	ACCATCTCCCTGCGCAGGTGCCCTGGCTGGGTGAACTGTGTGATCGAAGACGAGGAGCG	4619
Qy	4623	ACGGGTAGGGGACAGTCTGGCCCTACTACTAGCGGGGGTGGCAAGGCCCTGCTGGT	4682
Db	4620	ACGGGTAGGGGACAGTCTGACGCTACTACTAGCGGGGGGTGGCAAGGCCCTGCGGGT	4679
Qy	4683	GTGTGGGCTCAGGTCTGCTGTGGTGGCGGCTGGAAGCCGGTGTGACCTGTGTACGAATG	4742

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Db 9360 GGAAGAGCTCGGCCGAAGCCGGSITCTACT 9392

RESULT 4
US-08-461-361-14
; Sequence 14, Application US/08461361
; Patent No. 5856134
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Wages, John
; APPLICANT: Young, Lavonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; TITLE OF INVENTION: Cloning Thereof
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,361
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/389,886
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,509
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,729
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,271
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,558
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,543
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,985

; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9392 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HGV-PNF 2161 Variant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 459..9077
; US-08-461-361-14

Query Match 84.9%; Score 7979; DB 2; Length 9392;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 8515; Conservative 1; Mismatches 876; Indels 1; Gaps 1;
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QY 243 GCTGGCCCTACCGGTGTGAATAAGGGCCGACGTCAGGCTCGCTTAAACCCGAGCCCGT 302
Db 241 GTTGGCCCTACCGGTGGGAATAAGGGCCGACGTCAGGCTCGCTTAAACCCGAGCCCGT 300
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QY 423 GACCCCAACCCCTGCCCTTCCCGGTGGCGGAAATGTCATGGGCGCACCCAGCTCCGCG 482
Db 420 GACTCCAAGTCCCGCCCTTCCCGGTGGCGGAAATGTCATGGGCGCACCCAGCTCCGCG 479
QY 483 CGGCGCTGCAGCCGGGGTAGCCCAAGAAATCCTCGGGTAGGGCGGGGTGCGATTCTCTT 542
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Db 780 GCGGCCCAACTGTTGGGAGCTGGGTAGCCTATACGGGCCCTGTCTCGGCTAT 839
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Db 840 GTGGCTGGGATCCTGGCCCTGGGTGAGGTGTACTCGGGTGTCTAACGGTGGGAGTCGG 899
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Db 900 TTTGACCGCGCGGTCTACCGGTGCTTAACCTGACCTGTGACGTGCGTGTGAGCTTAAAG 959
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Db 1020 TACCTCTGGAAGTCCCATTTGATTTCTGAGAGGCGTGATAAGCCTGACCCCTTGTG 1079
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QY 1863 CGGATTCCTCTGATTTGGTGAATGTCCACACCAAGCCATAGAGCTCCGACTGGAACG 1922
Db 1860 CGAGATACCTTACATCTGTGGAGTGTCCACACCAAGCCATGAGCTCCACCGGAGC 1919
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Db 1920 TTTGGGTTCCTCCCGAGTTCGCGCCATTAACAACCTGCAATGCCGTAGCAGCGAAGTG 1979
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Db 6120 AGGAGCCTAAGGTGGATGAGTACAGGTGGGGTATGTCTGGGACCTGTGGGAGTGGATC 6179
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Db 6660 CCGTGGCAAAAGTGTTCACATTTGACGCGGAGCGCTACACCTTGCCTCATCACTGAGGCTC 6719
QY 6723 AGGAATGCGGCGCTCTGAGGTGTCATCCGAGGTGTCATTTGACATTTGGGAGGAGACT 6782
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|||||

RESULT 5
US-08-485-910-14
; Sequence 14, Application US/08485910
; Patent No. 5874563
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu P.
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; APPLICANT: Young, LaVonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; TITLE OF INVENTION: Cloning Thereof
; NUMBER OF SEQUENCES: 277
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; CITY: Palo Alto
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; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,910
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/389,886
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,509
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,729
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,271
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,558
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,543
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,985
; FILING DATE: 20-MAY-1994
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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9392 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: HGV-PNF 2161 Variant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 459..9077
US-08-485-910-14

Query Match 84.9%; Score 7979; DB 2; Length 9392;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 8515; Conservative 1; Mismatches 876; Indels 1; Gaps 1;
QY 3 ACGTGGGGGTTGATCCCCCCCCCGGCACACTGGGTGCAAGCCCATATAAACCGAGCCT 62
Db 1 ACGTGGGGGAGTTGATCCCCCCCCCGGCACACTGGGTGCAAGCCCATATAAACCGAGCCT 60
QY 63 ATCTAAGTAGACGCAATGACTCGGCGCGGACTCGGCGACCGCCCAAAAGGTGGTGATGG 122
Db 61 ATCTAAGTAGACGCAATGACTCGGCGCGGACTCGGCGACCGCCCAAAAGGTGGTGATGG 120
QY 123 GTGGTGACAGGGTTGGTAGTCTGCTAAATCCCGGTTCATCTGGTAGCCACTATAGTGGGT 182
Db 121 GTGATGACAGGGTTGGTAGTCTGCTAAATCCCGGTTCATCTGGTAGCCACTATAGTGGGT 180
QY 183 CTTAAGAGAAGGTCAAGACTCTCTTGTGCTGGGCGAGACCGGCGACGGTCCACAGGT 242
Db 181 CTTAAGAGAAGGTCAAGACTCTCTTGTGCTGGGCGAGACCGGCGACGGTCCACAGGT 240
QY 243 GCTGCCCCCTACCGGTGTGAATAAGGGCCGACGTGAGTCTGCTGTTAAACCGAGCCCGT 302
Db 241 GTTGGCCCTACCGGTGGGAATAAGGGCCGACGTGAGTCTGCTGTTAAACCGAGCCCGT 300
QY 303 CACCCACCTGGCAAAACGACGCCACGTACCGTCCACGTCCGCCCTTCAATGTCTCTTTG 362
Db 301 TACCCACCTGGCAAAACGACGCCACGTACCGTCCACGTCCGCCCTTCAATGTCTCTTTG 360
QY 363 ACCAATAGTTTATCCCGCGAGTTGACAAGGACCAAGTGGGGCGCGGGGTATGGGGAAG 422
Db 361 ACCAATAGGCGTAGCGCGGAGTTGACAAGGACCAAGTGGGGCGCGGGGT-TGGAGAGG 419
QY 423 GACCCCAACCCCTGCCCTTCCCGGTGGGCGCGGGAATGCATGGGCGCACCGACTCCCGG 482
Db 420 GACTCCAAGTCCCGCCCTTCCCGGTGGGCGCGGGAATGCATGGGCGCACCGACTCCCGG 479
QY 483 CGGCCTGCAGCGGGGTAGCCCAAGAAATCCTTCGGGTGAGGGCGGGTGGCAATTTCTTT 542
Db 480 CGGCCTGCAGCGGGGTAGCCCAAGAAATCCTTCGGGTGAGGGCGGGTGGCAATTTCTTT 539
QY 543 TTCTATACCATCATGGCAGTCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 602
Db 540 TTCTATACCATCATGGCAGTCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 599
QY 603 GCGCGCGCCACCGCTTGTGCGAGCGAATGGCGAATATTCCTCACAAATGCTGTGCC 662
Db 600 GCGCGCGCCACCGCTTGTGCGAGCGAATGGCGAATATTCCTCACAAATGCTGTGCC 659
QY 663 CCGGAAGACATCGGGTCTGCTGCTGGAAGCGGATGCCTGTGGTGGCGCTGGGGTGCACGGTT 722
Db 660 CCGGAGGACATCGGGTCTGCTGCTGGAAGCGGATGCCTGTGGTGGCGCTGGGGTGCACGATT 719
QY 723 TGCACCGCAGCTTGTGCGCCACTGTATCAGGCGGGTTTGGTGTGCGGCCCTGGCAAGTCC 782
Db 720 TGCATGACCAATGCTGCGCCACTGTATCAGGCGGGTTTGGTGTGCGGCCCTGGCAAGTCC 779
QY 783 GCGGCCAGCTCGTTGGGGAAGTGGGAGCGCTGTACGGGGCCCTTCTCGGTCTCGGCTTAC 842
Db 780 GCGGCCAAGTGGTGGGGAGCTGGGTAGCCCTATATACGGGGCCCTTCTCGGCTTAC 839
QY 843 GTAGCGGGATCCTGGGTCGTGGGCGAGGTCTACTCCGGGGTCTCACAGTTGGTCTTGGC 902
Db 840 GTGGCTGGGATCCTGGGCTGGTGGAGGTGACTCGGGTGTCTTACCGGTGGGAGTCCGG 899
QY 903 TTGAGGCCCGCGGTCTACTGTATGCCCAACCTGAAGTGTGCAGTAGAATGACGCTTAAG 962
Db 900 TTGAGCGCGCGGTCTACCCGGTGCCTAACCTGACGTGTGCAGTGCCTGTGAGCTAAAG 959
QY 963 TGGGGAAGTGTGAGTTGGAGATGACTGACGAGTTGGCCCTCAATTTACTGATTTTGGAA 1022
Db 960 TGGGAAAGTGTGAGTTGGAGATGACTGACGAGTTGGCCCTCAATTTACTGATTTTGGAA 1019
QY 1023 TACCTTTGGAAAGTCCCATTTTGAATTTTGGAGAGGAGTGATGAGCCTTGACCCCTCTGTTG 1082

Db	5400	GTGTTGTCTTGGCTCAGGCTAAGACGGCGGAGGCTTACACAGCAACCGCCAGTGGCTC	5459
Qy	5463	GCTGGCTGCTACACGGGAGCGGGCGCTCCACCAGTGTTCATTTGTTGTGACAAAGCTCTTC	5522
Db	5460	GCTGGCTGCTATACGGGAGCGGGCGGCTCCACTGTATCCATTTGTTGACAAAGCTCTTC	5519
Qy	5523	GC GGCGGCTGGCGCGCGGTGTAGGCCATTGCCACAGTGTAAATAGCTGCGGCAGTGGCG	5582
Db	5520	GC GGAGGCTGGCGCGCTGTGTGGGCCATTGCCACACGCTGATTTGCTGGCGGCTGGCG	5579
Qy	5583	GCCTATGGGCTTCTAGGAGCCCTCCATTTGGCTGCTGCCGCTTCCCTACCTCATGGGGTTG	5642
Db	5580	GCCTACGGGCTTCTAAGAGACCGCGCTTGGCAGCGCGGCTTCCCTACCTCATGGGGTTG	5639
Qy	5643	GGCTGCGAGGCAACGCGAAACCGCTTAGCGCTCCGCTCTCTCTACTAGGGCGCGCTGGG	5702
Db	5640	GGCGTTGGAGGAACCGCTCAGACGCGCTGGCGCTGCCCTCTCTATTGGGGGCTGCTGGA	5699
Qy	5703	ACCGCTTGGGCAACGCTGCTGTGGGGTTAACCATGGCGGGCGGCTTCATGGGAAGTCT	5762
Db	5700	ACCGCTTGGGCACTCTGCTGTGGCTTGACCATGGCAGTGGCTTCTATGGGGGGGCGC	5759
Qy	5763	AGCGTCTCCCGCTCTTGTGTACCACTTTTACTGGGGGCGGCTGGGGGCTGGGAGGGCTG	5822
Db	5760	AGTGTCTCCCGCTCTTGTGTACCACTTTTATTGGGGGCGGCTGGAGGTTGGGAGGTT	5819
Qy	5823	GTGAATCGCGCTAGCTTGTCTTGACCTTATTATGGGGGGAACATCATCAGAAAGATCTG	5882
Db	5820	GTCAACCGCGGAGCCTAGTCTTTGACTTATGGCGGGGAACCTTCTCATCAGAAAGATCTG	5879
Qy	5883	TGTPATGCCATCCCACTGTCTAACCACTGCGGGGCGAGCACTTGGGGGATGCGCCCTCGG	5942
Db	5880	TGGTATGCCATCCCGTACTGTACACGCGGGGCGGGCCCTTGGGGGATCGCTCTCGG	5939
Qy	5943	TTGGTGTGTACTCAGCTAACAACTCTGCACTACCACTTGGTTGAACTCTGCTCACT	6002
Db	5940	TTGGTTTGTATTACGCTAACAACTCTGCACTACCACTTGGTTGAACTCTGCTCACT	5999
Qy	6003	ACATTGCCAAGTCTCATGCTACCTGACACTTACTTTTCAGCAGGCGGATTACTGTGAC	6062
Db	6000	ACGTTACCAAGTCTTCATGTATCCGGGACACTTACTTTCAGCAAGTTGACTATTGGCAC	6059
Qy	6063	AAGTCTCAGCTGTGTCGACGCTTGAGCCTCACTCGCACCGTGGTTGCCCTGGTCAAC	6122
Db	6060	AAGTCTCAGCGTGTCCGGCGCTGAGCCTCACCCGCACAGTGGTTGCCCTGGTCAAC	6119
Qy	6123	AGGAGCCTAAGTGTGATCAGTTTCAAGTGGGGTACGCTCTGGGACTTGTGGGAGTGATC	6182
Db	6120	AGGAGCCTAAGTGTGATCAGTTACAGTGGGGTATGTTGGGACCTTGTGGGAGTGATC	6179
Qy	6183	ATGGCTCAAGTGGCATGTGTATGGCCAGACTTGGGCGCTCTGCCCGTGGTGTCAATTA	6242
Db	6180	ATGGCCCAAGTGGCGTGTGTATGGCCAGACTCAGGGCGCTCTGCCCGTGGTGTCACTA	6239
Qy	6243	CCCTTATGGCACTCGGGGAGGGTGGTCCGAGAAATGGTTGTTGGACGGCCATGTTGAG	6302
Db	6240	CCCTTGTGGCATTCGGGGAGGGTGGTCCGSGGAATGGTTGCTTGACGTCATGTTGAG	6299
Qy	6303	AGTCGTTGTCTTTGTGGTTGCGTGATCATCCGGTGTGATTTTGAATGGGCACTCAAAAGT	6362
Db	6300	AGTCGTCGCTCTGTGGCTGCGTGATCATCTGTGTGAGTTCTGAATGGGCACTCAAAAG	6359
Qy	6363	CCAGTTTACTCTACCAAGCTGTGCAGGCATTTATGGATGGGGACAGTCCCTGTGAACATG	6422
Db	6360	CCAGTTTACTCTACCAAGCTGTGCAGGCATTTATGGATGGGGAGTGTCCCTGTGAACATG	6419
Qy	6423	CTGGGCTATGGCAGACGCTCGCTTTGCTGCGCTCAGACACCCCGAAGGTGGTACCATTC	6482
Db	6420	CTGGGTTACGGTGAACGCTCGCTCTCTCTGGCTCCGACACCCCGAAGGTGTGCCCTTC	6479
Qy	6483	GGGACGCTCTGGGTGGGCTGAGTGGTGTGACCCCTACCCACGTTGTGATCAGGCGAACA	6542

Db	6480	GGGAGCTCTGGCTGGGGCTGAGGTGGTGGACCACTACCCACGTGGTAAATCAGAGGAGACC	6539
Qy	6543	TCCGCCTACAACTGCTGCGCCAGCAAAATCCTGTGCGCTGCTGTGTTCTCTGAGCCCTATTATAC	6602
Db	6540	TCCGCCATTAGCTGCTGCGCCAGCAAAATCCTATCGCTGCTGTAGCTGAGCCCTACTAC	6599
Qy	6603	GTCAGCGCATACCGGTCTCATGGGACGGGAGCGCGAGCGCCGTGCATGGTCTATGGC	6662
Db	6600	GTCAGCGCATTCGGGTCTCATGGGACGGGAGCGCTGTCGCGCGCGCCATGTGCTCTATGGC	6659
Qy	6663	CCTGGCAAAAGTGTCAACATTGACGGGAAACGCTACACCTTTCCGCATCAACTCGCGGCTT	6722
Db	6660	CCTGGCAAAAGTGTACATTGACGGGAGCGGTACACCTTGCCCTATCAACTCAGGCTG	6719
Qy	6723	AGGAATGTGGCGCCTCTGAGGTGTCATCCGAGGTGTCCATTACATTTGGGACGGAGACT	6782
Db	6720	AGGAATGTGGCACCCCTCTGAGGTTTCATCCGAGGTGTCCATTGACATTTGGGACGGAGACT	6779
Qy	6783	GAAGACTCAGAACTGACTGAGCGCGACCTGCGCGCGCGCGCTGCGAGCCCTTCAGGCTATC	6842
Db	6780	GAAGACTCAGAACTGACTGAGCGCGGATGCGCGCGCGCGCTGCTCTCTCCAAACGGCATC	6839
Qy	6843	GAGAACTCTCGGAAATTCCTTGAACCTCACAATAGATGTCAATCATGGAAGATTTGCAGTACA	6902
Db	6840	GAGAACTCTCGGAGATTCCTTGAACCGCATTTGATGTCAATCATGAGAGCTGCAAGTACA	6899
Qy	6903	CCCTCTCTTTGTGGAGTAGCCGAGAGATGCCCTGTGTGGGGAGAGACATACCCCGCACT	6962
Db	6900	CCCTCTCTTTGTGTAAGTACCCGAGAGATGCCCTGTATGGGAGAGACATCCCCGTACT	6959
Qy	6963	CCATCGCCAGACATTATCTCGGTTACTGAGAGCAGCCAGATGAGAAGACCCCGTCGGTG	7022
Db	6960	CCATCGCCAGACATTATCTCGGTTACTGAGAGCAGCTCAGATGAGAAGACCCCGTCGGTG	7019
Qy	7023	TCCTTCTCTCGAGGAGATACCCGCTCTCTGACTCAATTCAGAGTCAATCCAGAGTCCCGAG	7082
Db	7020	TCCTTCTCTCGAGGAGATACCCGCTCTCTGACTCAATTCAGAGTCAATCCAGAGTCCCGAG	7079
Qy	7083	ACAGCCGAAGGGAGGAAAGCGTCTTCAACGTGGCTTTTCCGTACTTAAAGCCCTTGTTT	7142
Db	7080	ACAGCCGAAGGGAGGAAAGTGTCTTCAAGTGGCTTTTCCGTATTAAAGCCCTTATTT	7139
Qy	7143	CCACAGAGCATGCCACAAGAAAGCTTACGGTTAAGATGTCATGCTGTGTGTGAGGAAGAC	7202
Db	7140	CCACAGAGCAGCGGACCGAGGAAGCTTACCGTCAAGATGCTGCTGTGGGTTGAAAGAGC	7199
Qy	7203	GTAACGCTCTCTTTTCATTGGGATTCAGGTCGCTGAGCTGGCAAGCTGTGTGAGATG	7262
Db	7200	GTCACGGGCTTTTCTCATTTGGGGTGTAGCGGTGGCTGTGTTGTGCTAGGCTGTGTGAGATG	7259
Qy	7263	GAATCCAGAACCATACAGCCTATTGTGACAAGGTGCGCACTCCGCTTGAATTGACAGGTT	7322
Db	7260	GAATCCAGAACCATACAGCCTATTGTGACAGGTGCGCACTCCGCTTGAATTGACAGGTT	7319
Qy	7323	GGGTCTTGGTGGCAATGAACCTTACCTTTGAATGTGACAAGTGTGAGCTAGGCAAGAG	7382
Db	7320	GGGTCTTGGTGGCAATGAACCTTACCTTTGAATGTGACAAGTGTGAGGCTAGGCAAGAA	7379
Qy	7383	ACCTTGGTTCCTTCTCTTACATTTGGTCTGGGTGCCACTGACAGGGGCCACTCCGCCC	7442
Db	7380	ACCTTGGCTCCTTCTCTTACATTTGGTCTGGAGTGCCTGACTAGGGCCACGCGCGCC	7439
Qy	7443	AAGCCCCCTGTGTGAGGCGGTTGGCTCTCTGCTGTCGTCGCGCACACCAAGAGTGTAT	7502
Db	7440	AAGCCTCCGCTGTGTGAGGCGGTTGGCTCTTGTGTAGTGGCCGACACTACTAAGGTGTAT	7499
Qy	7503	GTCACCAACCCGACAAATGTTGGGAGAAAGTTGACAAGGTTTACCTTCTTGGCGTGCCTCT	7562
Db	7500	GTTACCAATCCAGACAAATGTGGCAGGAGGTTGACAAGGTGACCTTCTTGGCGTGCCTCT	7559
Qy	7563	AGGGTTCATGACAAATTCCTCTGTGGACTCCATAGAGCGCGCTTAAGAGGCGACTCAAGCC	7622
Db	7560	AGGGTTCATGATAGTATCTCTGAGTCTCTATTGAGCGCGCTTAAGAGGCGCGCTCAAGCC	7619

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 38,443
REFERENCE/DOCKET NUMBER: 4600-0124
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9391 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: PNF-2161 genome
FEATURE:
NAME/KEY: CDS
LOCATION: 459..9077
US-08-638-911A-1

Query Match 84.9%; Score 7971.8; DB 1; Length 9391;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 8509; Conservative 0; Mismatches 877; Indels 1; Gaps 1;

QY	723	TGCACGACCGCTTGTGCTGGCCACTGTATCAGGGGGTTTGGCTGTGGGCTTGGCAAGTCC	782
DB	720	TGCACTGACCAATGCTGGCACTGTATCAGGGGGTTTGGCTGTGGGCTTGGCAAGTCC	779
QY	783	GGGGCCCACTGTTGGGGAACCTGGGAGCCCTCTACGGGCCCCCTTCGCTCTCGGCTTAC	842
DB	780	GGGGCCCAACTGTTGGGAGCTGGGTAGCCCTATACGGGCCCCCTTCGCTCTCGGCTTAT	839
QY	843	GTAGCCGGATCTCTGGGTCTGGCGAGGTTTACTCCGGGTCTCTGACAGTGTGGTGTGGG	902
DB	840	GTGGCTGGGATCTCTGGGCTGGGTGAGGTGTACTCGGGTCTCTACGCTGGGAGTTCGG	899
QY	903	TTGAGCCCGGGTCTACCTGATGTCACCAACCTGAAGTGTGACAGTAGAATGTGACGTTAG	962
DB	900	TTGAGCCCGGGTCTACCCGGTGCCTAACCTGACGTGTGACGTGCTGAGCTAAAG	959
QY	963	TGGGGAAGTGAAGTTTGGAGATGGACTGAGCAGTTGGCCCTCCCAATTTACTTGGATTTGGAA	1022
DB	960	TGGGGAAGTGAAGTTTGGAGATGGACTGAACAGCTGGCCCTCCCAACTTACTTGGATTTGGAA	1019
QY	1023	TACCTTTGAAAGTCCCATTTGAATTTTGGAGAGGATGATGAGCCTGACCCCTCTGTGTG	1082
DB	1020	TACCTCTGGAAGTCCCATTTGATTTCTGGAGAGGCGTGTATAGCCTGACCCCTTGTGTG	1079
QY	1083	GTTTGGGTGGCCGCAATTTGCTTGGAGCAACGGATTGTCTATGTTTTCCTGTGGTG	1142
DB	1080	GTTTGGGTGGCCGCAATTTGCTTGGAGCAACGGATTGTCTATGTTTTCCTGTGGTG	1139
QY	1143	ACGATGGGGGAGTGTGCAAGCGCCCGCTCCGTTTGGGGTCCCGCCCTTTGAC	1202
DB	1140	ACGATGGGGGAGTGTGCAAGCGCCCGCTCCGTTTGGGGTCCCGCCCTTTGAC	1199
QY	1203	TAGGGGTGAGTGGGAGTCACTCTCTGAGGGCTAAGGGTCTGCTATTTCCACTGGG	1262
DB	1200	TAGGGGTGAGTGGGAGTCACTCTCTGAGGGCTAAGGGTCTGCTATTTCCACTGGG	1259
QY	1263	GAGAGGTTGGGATCGAGGGAATGTACGCTCTTGTGTGACTGCCCAACGGCCCTTG	1322
DB	1260	GAGAGGTTGGGATCGAGGGAATGTACGCTCTTGTGTGACTGCCCAACGGCCCTTG	1319
QY	1323	GTTTGGTCCCGCCCTTTTGGCAGGCGTGGGTGGGGGACCCCATCACCATTGGAGC	1382
DB	1320	GTTTGGTCCCGCCCTTTTGGCAGGCAATCGGCTGGGGTACCCCATCTATTTGGAGC	1379
QY	1383	CACGACAAACACAGTGGCCCTTATCATGCCCAATATGCTATGGGTCTGTGCTCGTA	1442
DB	1380	CACGACAAACACAGTGGCCCTTATCATGCCCAATATGCTATGGGTCTGTGCTACAGTC	1439
QY	1443	ACGTGCTGTGGGTTCCGTTGCTTGGTTCGCTCGACCGCGGTGCTGATTCGAGATC	1502
DB	1440	ACGTGCTGTGGGTTCCGTTGCTTGGTTCGCTCGACAGTGTGCTGCTGCGACTCGAAGATA	1499
QY	1503	GATGTTGAGTGTGGTGGCGGTGGATCTGCCAGCTGACCATAGCCCTCTAGGGTCA	1562
DB	1500	GATGTTGAGTGTGGTGGCGGTGGATCTGCCAGCTGACCATAGCCCTCTAGGGTCA	1559
QY	1563	TCGGATCGGACACAGTGGTGTGAGTCTCCGAGTGGGAGTCCCGTCCGTAAGCTGTATT	1622
DB	1560	TCGGATCGGACACAGTGGTGTGAGTCTCCGAGTGGGAGTCCCGTCCGTAAGCTGTATT	1619
QY	1623	CTGACCGCTGGGCTGCTTATGTGGCACTGTGTGGGAGTGTGCTGGGCCGAACCGGG	1682
DB	1620	CTGACCGCTGGGCTGCTTATGTGGCACTGTGTGAGGAGTGTGCTGGGCCGAACCGGG	1679
QY	1683	TCGGTTAGATTTCCTTCCATCGGTGGGACCGGGCTCGGCTGACAAAGGACTTGGAA	1742
DB	1680	TCGGTTAGATTTCCTTCCATCGGTGGGACCGGGCTCGGCTGACAAAGGACTTGGAA	1739
QY	1743	GCCTGCTCTCCTCAACAGGCAACTCCCTTCCATTAAGGGGCCCCCTTGGGCAACAG	1802
DB	1740	GCCTGCTCTCCTCAACAGGCAACTCCCTTCCATTAAGGGGCCCCCTTGGGCAACAG	1799

QY	3	ACGTGGGGGTTGATCCCGCCCGGACCTGGGTGCAAGCCCATAAACCGACGCT	62
DB	1	ACGTGGGGGTTGATCCCGCCCGGACCTGGGTGCAAGCCCATAAACCGACGCT	60
QY	63	ATCTAAGTAGACCAATGACTCGGCGGACCTCGGGGACCGGCCAAAGGTGTGGATGG	122
DB	61	ATCTAAGTAGACCAATGACTCGGCGGACCTCGGGGACCGGCCAAAGGTGTGGATGG	120
QY	123	GTGGTGACAGGTTGTAGTCTGTAATCCCGGTCTATCTGTGAGCCACTATAGTGGGT	182
DB	121	GTGATGACAGGTTGTAGTCTGTAATCCCGGTCTATCTGTGAGCCACTATAGTGGGT	180
QY	183	CTTAAGAGAGGTCAGACCTCTTGTGCTCGGCGACCGCGACCGGTCACAGGT	242
DB	181	CTTAAGAGAGGTCAGACCTCTTGTGCTCGGCGACCGCGACCGGTCACAGGT	240
QY	243	GCTGGCCCTACCGGTGTGAATAAGGGCCGACGTCAGGCTCTGTTAAACCGAGCCGT	302
DB	241	GCTGGCCCTACCGGTGTGAATAAGGGCCGACGTCAGGCTCTGTTAAACCGAGCCGT	300
QY	303	CACCCACTGGGCAACGACGCGCCAGTACGCTGACGCTCGGCTCTCTCTTG	362
DB	301	TACCCACTGGGCAACGACGCGCCAGTACGCTGACGCTCGGCTCTCTCTTG	360
QY	363	ACCAATAGGTTTATCCGGCGAGTTGACAAGGACAGTGGGGGCGGGGTTATGGGAAG	422
DB	361	ACCAATAGGCGTAGCCGCGAGTTGACAAGGACAGTGGGGGCGGGGCT-TGGAGAGG	419
QY	423	GACCCCAACCCCTGCCCTTCCCGTGGGCGGGAATGATGGGCGCACCCAGCTCCGCG	482
DB	420	GACTCCAAGTCCCGCTTCCCGTGGGCGGGAATGATGGGCGCACCCAGCTCCGCG	479
QY	483	CGGCGCTGACGCGGGGTAGCCCAAGAAATCTTCGGGTGAGGGGGGTGCAATTTCTTT	542
DB	480	CGGCGCTGACGCGGGGTAGCCCAAGAAATCTTCGGGTGAGGGGGGTGCAATTTCTTT	539
QY	543	TTCTATACCATGAGCAGTCTCTGCTCTCTGCTGCTGAGGCGGGGCAATTCG	602
DB	540	TTCTATACCATGAGCAGTCTCTGCTCTCTGCTGCTGAGGCGGGGCAATTCG	599
QY	603	GCCCGGCCCAACCGCTTGTGAGGCAATGGCAATTTCTTCAAAATGCTGTGCC	662
DB	600	GCCCGGCCCAACCGCTTGTGAGGCAATGGCAATTTCTTCAAAATGCTGTGCC	659
QY	663	CCGGAAGACATCGGGTCTGCTGGAAGGCGGATGCTGCTGGCCCTGGGGTGCAGGTT	722
DB	660	CCGGAAGACATCGGGTCTGCTGGAAGGCGGATGCTGCTGGCCCTGGGGTGCAGGTT	719

Db 3960 GGTAAACATCAAGTATATACCTGTGGCGATGATACAACCTGCTTTCCACAAGGATCACTGAC 4019
Qy 4023 TCGCCCTTACCTATTCCACTTACGGAAGTTTGGCCAAACCTAGGCAGATGCTGAGG 4082
Db 4020 TCCCCCTGACGATTTCAACCTATGGAGTTTGGCCAAACCTTAGGCAGATGCTACGG 4079
Qy 4083 GGTGTGTCGGTGGTCAATTTGTGACGAGTGCCACAGTCATGACTCAACTGTGTTGGGG 4142
Db 4080 GCGTTTCGGTGGTCAATTTGTGATGAGTGCCACAGTCATGACTCAACCGTGTGTTAGGC 4139
Qy 4143 ATTGGCGTGTGAGGAGCTGCGGCGAGGATGTGAGTGCAATTTGGTGTCTACGCCACT 4202
Db 4140 ATTGGAGAGTCCGGAGCTGCGGCTGAGGAGCGGCTGCAACTAGTGTCTTACGCCACC 4199
Qy 4203 GCCACCCCTCCGGATCCCGATGACCAGCACCCATCAATCATTGAGACAAATGGAC 4262
Db 4200 GCTACACCTCCCGATCCCTTATGACGACGACCCCTTCATTAATTGAGACAAATTTGAC 4259
Qy 4263 GTGGAGAGATCCCTTCTATGGGCATGGCATACCTCTTTGAGCGGATCGGACCGAAAG 4322
Db 4260 GTGGGAGATTCCTTTATGGGCATGGAATACCCCTCGAGCGATGCGAACCGAAGG 4319
Qy 4323 CATCTGCTATTGCGCATCCAAAGCTGAGTGGAGCGCTCGGCGGCGCAGTTTCGGCT 4382
Db 4320 CACCTCGTGTCTGCCAATCTTAAGCTGAGTGGAGCGCTTGTCTGGCAGTTCTCCGCT 4379
Qy 4383 AGGGGGTAAATGCCATCGCCTATTACAGGGGGAAGACAGTTCTATCATCAAGATGA 4442
Db 4380 AGGGGGTCAATTGCCATTTGCTATTATAGGGGTAAGACAGTTCTATCATCAAGGATGG 4439
Qy 4443 GACCTGGTGTGTGCTACAGACGACATATCCACTGGGTGACACTGGAACTTCGATTCT 4502
Db 4440 GACCTGGTGTGTGCTACAGACGCGCTTCCACTGGGTGACACTGGAAATTTTCGACTCC 4499
Qy 4503 GTCACCGATTGGTGTAGTGTGAGGAGGTCGTCGAGGTGACCTTGATCCACCATT 4562
Db 4500 GTCACCGACTGGGATTAAGTGTGAGGAGGTCGTTGAGGTGACCTTGATCCCACTT 4559
Qy 4563 ACCATCTCCCTCGCAGGTGCGCGCTCGGCTGAACCTGTCATGACGCGGAGAGCG 4622
Db 4560 ACCATCTCCCTCGGACAGTGCCTGGCTGGCTGAACTGTCATGCAAGAGAGAGCG 4619
Qy 4623 ACGGTAGGGGAGGTCTGTGGCGCTTACTACTACGCGGGGTGCGAAGCCCTCTGCTGT 4682
Db 4620 ACGGTAGGGGAGGTCTGTGGCGCTTACTACTACGCGGGGTGGGCAAGCCCTCGGCT 4679
Qy 4683 GTGTGCGCTAGTCTGCTGTGTCGGGTGAGCGGTGACCTGGTACCGAATG 4742
Db 4680 GTGTGCGCTCAGGTCCTGTCTGTGTCGGGTGGAAGCTGGAGTGACCTGGTACGGAATG 4739
Qy 4743 GAACTGACTGACAGCAAACTACTGAGACTTTACGACAACTGCGCTTACACCGCAGCC 4802
Db 4740 GAACTGACTGACAGCTAACCTACTGAGACTTTACGACGACTGCGCTTACACCGCAGCC 4799
Qy 4803 GTCGAGCTGACATTTGGGAAGCCCGGTGTTCTTTTCGGGCTGTGCCCGTGTAGGATG 4862
Db 4800 GTCGCGGCTGATATCGGAAGCCCGGTGTTCTTCTCTGGCTCGCCCATTTGAGGATG 4859
Qy 4863 CATCCGATGTTAGCTGGCAAACTGCGCGCTCACTGCGCTTCTGCTGGTGGTGT 4922
Db 4860 CACCTGTATGTCAGCTGGCAAAATGTCGCGCGCTCACTGCGCTTCTTGGTGGTGT 4919
Qy 4923 CAGCGACCATGTGCGGGAACACTGTCTCCCGGCCATCGATGACCCCGAGTGGCA 4982
Db 4920 CAGCGACCATGTGCGGGAACACTGTCTCCCGGCCATCGATGACCCCGAGTGGCA 4979
Qy 4983 GGTCTGAGGGCCGAATCTCTCCACTCTCTGCTGAGTGGGGCAATGATTTACATCT 5042
Db 4980 GGTCTGAGGGCCGAATCTCTCTCACTCTCTGCTGAGTGGGGCAATGATTTACATCT 5039
Qy 5043 AAGGTGGCGGCCATACATCTGTGACGACCTGTGTCGCTGAGCTGGGTGCGGAGGT 5102
Db 5040 AAGGTGGCGGCCACCATATAGTGGACACCTGGTCCGAGACTCGGTGGCGGAGGT 5099

Qy 5103 TACGTCCCTGCGATGCGGACCCCATCTTGATGTGGCTCGCTATTTCGGGGGCGCATG 5162
Db 5100 TACGTCCCTGCGAGCTGGCCGATCTTGATGTCGCTAGCTATTCGGGGGGAATG 5159
Qy 5163 ATCTATGCGTCAATACACCGGGTCTCTGTTGGTTTACAGACTGGGATGTGAAGGGGT 5222
Db 5160 ATCTACGCGTCAATACACCGGGTCTGTTGGTGTGACAGACTGGGATGTGAAGGGGT 5219
Qy 5223 GCGACCCCTTTATCGCATGGAGCCAGCCACGCGCCCGGCTTGTGCAGTCC 5282
Db 5220 GCGCCCTTTATCGCATGGAGCCAGCCACGCTCAGCCGCTGGTGCAGTCT 5279
Qy 5283 CCGGTAGACCATCGCGGGGAGTCTGCGCATCGGATCGGATGCCAACACAGTGACAGT 5342
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Db 5460 GCTGCTGCTATACGGGACGCGGCGCTGCCACTGTATCCATGTTGACNAAGTCTTC 5519
Qy 5523 GCGGGGCTGGGCGCGTGTAGGCCATTGCCAGTGTAAATAGCTGCGGACGTGGG 5582
Db 5520 GCGGAGGTGGGCGCTGTGGTGGCCATTGCCACAGCGTGTATGCTGCGGCGTGGG 5579
Qy 5583 GCCATGGGGCTTACAGAGCCCTCCATTGGCTGCGGCTTCTACTAGGGCCCTGGG 5702
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Qy 5763 AGCTCTCCCTCTGCTGCTACCATTTTACTGGGCGCGTGGGGGCTTGGAGGCGCTG 5822
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Db 6000 ACATTGCCAAGTCTCTATGATATCCCGGACAGTTACTTTCAGCAAGTTGACTATTTCGAC 6059
Qy 6063 AAGTCTCAGCTGTGCTCCGAGCTTACGCTCAGCTCAGCTGCTGGTGGTGGTCAAC 6122
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Qy 6123 AGGAGCTAAGGTGATGAGTTTCCAGTGGGTACGCTTGGGACTTGTGGAGTGGATC 6182
Db 6120 AGGAGCTAAGGTGATGAGTTTCCAGTGGGTATGCTGGGACTTGTGGAGTGGATC 6179

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Qy	8403	CCTTCGTATCATGCATCACTGGACACGGCCCCCTTCTGCTCCACTTGGCTAGCTAGTGA	8462
Db	8400	CCCTCATATCATGCATATTGGACAGGCCCCCTTCTGCTCCACTTGGCTAGTGA	8459
Qy	8463	AATGCAGAGGGGAAACGCCATTTCTCTTGACACCGGACTTTTCGGAGGCCCCCTCGCTCGC	8522
Db	8460	AATGCAGATGGGAAGCGCCATTTCTCTTGACACCGGACTTCCGGAGGCGCTCGCTCGC	8519
Qy	8523	ATGTGAGCAGGTACAGTACCAATAGGCTTCGGCCATCGGTTACATCTCTCTATACCTT	8582
Db	8520	ATGTGAGTGAATATAGTACCCGATGGCTTCGGCGATCGGTTACATCTCTCTTATTCCT	8579
Qy	8583	TGGCATCTATCACCGGTGGGTCAATCCCTCACGTGCTCACTGCGCGTTTAGGGT	8642
Db	8580	TGGACCCCATCACGGTGGGTATCATCCCTCATGTGCTAAAGTGGCATTCAGGGGT	8639
Qy	8643	GGTGGCACACCGTCTGATCTCTGTGTGGTGCCAGGTACATGGTAATTACTACAAGTTTCCA	8702
Db	8640	GGAGGCACACCGTCTGATCCGGTTTGGTGCCAGGTGCATGGTAAGTACTACAAGTTTCCA	8699
Qy	8703	CTGGACAACTGCCTTAACATCATGCTGGCCCTCCACGACACAGAGCGTTGAGGGTTACC	8762
Db	8700	CTGGACAACTGCCTTAACATCATGCTGGCCCTCCACGACACAGAGCGTTGAGGGTTACC	8759
Qy	8763	GCAGACAACTAAGACAAAAATGGAGGCTGGCAAGGTGCTGAGCGACCTCAAGCTCCCT	8822
Db	8760	GCAGACAACTAAGACAAAGATGAGGCTGTAAGTTCTGAGGGACCTCAAGCTCCCT	8819
Qy	8823	GGCCTAGCATCCACCGGAAGACCGGGGCATTTGCGAACCGATATGCTCCGGTCCGCG	8882
Db	8820	GGCTTAGCAGTCCACCGAAAGACCGGGGCGTTGGCAACACGATGCTCCGCTCGCG	8879
Qy	8883	GGTTGGGCTGAGTTGGCTAGGGGCTGTTGTGGCGTCCAGGCTTCGCGCTCCCGCTCG	8942
Db	8880	GGTTGGGCTGAGTTGGCTAGGGGCTGTTGTGGCATCCAGGCTTCGCTCCCGCT	8939
Qy	8943	GAGATTCTGTTATCCCGGGGTTTCCCGCTTCCCGCTTATATGGGGGTGGTTTCAT	9002
Db	8940	GAGATTGCTGTTATCCCGGGGTTTCCCTCTCTCCCGCTTATATGGGGGTGGTACAT	8999
Qy	9003	CAATTGGATTTCACAGCCAGAGAGTCGCTGGCGGTGGTTGGGTTCTTATAGCCCTGCTC	9062
Db	9000	CAATTGGATTTCACAGCCAGAGAGTCGCTGGCGGTGGTTGGGTTCTTATAGCCCTGCTC	9059
Qy	9063	ATCGTAGCCCTCTTCGGGTCAACTAAATTCATCTGTTCCGGCAGGCTCCGGTGACTGATC	9122
Db	9060	ATCGTAGCCCTCTTCGGGTCAACTAAATTCATCTGTTCCGCAAGGCTTGGTGACTGATC	9119
Qy	9123	ATCACTGGAGAGGTTCCCGCTCCCGCCCGAGGGTCTCCCGCTGGGTGAAAGGG	9182
Db	9120	ATCACTGGAGAGGTTCCCGCTCCCGCCCGAGGGTCTCCCGCTGGGTGAAAGGG	9179
Qy	9183	CCCGGCTTGGGAGGCATGGTGTACTAACCCCTTGGCAGGTCAAAGCTGATGGTGC	9242
Db	9180	CCCGGCTTGGGAGGCATGGTGTACTAACCCCTTGGCAGGTCAAAGCTGATGGTGC	9239
Qy	9243	TAATGACTCCACTTCGTTGGGGGTGCGTACCTTATAGCGTAAATCCGTGACTACGGGC	9302
Db	9240	TAATGACTCCACTTCGTTGGGGGTGCGTACCTTATAGCGTAAATCCGTGACTACGGGC	9299
Qy	9303	TGCTCGCAGAGCCCTCCCGGATGGGACAGTGCACATGTGATCTGAAGGGGTGCACCCC	9362
Db	9300	TGCTCGCAGAGCCCTCCCGGATGGGACAGTGCACATGTGATCTGAAGGGGTGCACCCC	9359
Qy	9363	GGTAAGAGCTCGGCCCAAGGCCGGGT	9389
Db	9360	GGGAAGAGCTCGGCCCAAGGCCGGTT	9386
RESULT 7			
PCT-US95-06266-14			

Db 61 ATCTAAGTAGACCAATGACTCGGCGCGGACCTCGCGACCGGCCAAAAAGGTGGTGGATGG 120
QY 123 GTGGTGACAGGTTGGTAGTGCCTAAATCCCGGTGCATCTGTGTAGCCACTATAGTGGGT 182
Db 121 GTGATGACAGGTTGGTAGTGCCTAAATCCCGGTGCATCTGTGTAGCCACTATAGTGGGT 180
QY 183 CTTAAGAGAAGTCAAGACTCCTCTGTGTGCTCGCGGAGAGCCGCGACGGTCCACAGGT 242
Db 181 CTTAAGAGAAGTCAAGACTCCTCTGTGTGCTCGCGGAGAGCCGCGACGGTCCACAGGT 240
QY 243 GCTGCGCCTACCGGTGTGAATAAGGCGCGGACGTCAGGCTCCTGTTAAACGAGCCCGT 302
Db 241 GTTGCCCTTACCGGTGGGAATAAGGCGCGGACGTCAGGCTCCTGTTAAACGAGCCCGT 300
QY 303 CACCACCTTGGGCAACGAGCCGACGTACGCTCCACGTCGCGCTTCAATGCTCTCTTG 362
Db 301 TACCACCTTGGGCAACGAGCCGACGTACGCTCCACGTCGCGCTTCAATGCTCTCTTG 360
QY 363 ACCAATAGGTTTATCCGGCGAGTTGACAAGGACCAAGTGGGCGCGGGGTATGGGGAAG 422
Db 361 ACCAATAGGCGTAGCGCGGAGTTGACAAGGACCAAGTGGGCGCGGGGT - TGGAGAGG 419
QY 423 GACCCCAACCTTCCCTTCCCGGTGGCGCGGAAATGCATGGGCGCACCGACTCCGG 482
Db 420 GACTCCAAAGTCCCGCTTCCCGGTGGCGCGGAAATGCATGGGCGCACCGACTCCGG 479
QY 483 GCGGCTGCGAGCGGGTAGCCCAAGAAATCCTTCGSGTGAGGCGGSGTGCGCATTTCTCT 542
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QY 543 TTCTATACCATCATGCGACTCCTCTCTGCTCCTCTCTGTTGAGCGCGGGCCATTTCTG 602
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QY 663 CCGGAAGACATCGGTTCTGCTGCGAAGCGGATGCCGTGGCGGCTGGGTCGACGGTT 722
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Db 6540 TCCGCTTAAAGTCTGCTCGCCAGCAAACTCTATCGGCTGTGTAGCTGAGCCCTTATAC 6599
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QY 9303 TGCTCGCAGAGCCCTCCCGGATGGGACAGTGCACACTGTGATCTGAAGGGGTGCACCC 9362
Db 9300 TGCTCGCAGAGCCCTCCCGGATGGGACAGTGCACACTGTGATCTGAAGGGGTGCACCC 9359
QY 9363 GGTAGAGCTCGGCCCAAGCGCGGT 9389
Db 9360 GGTAGAGCTCGGCCCAAGCGCGGT 9386

RESULT 8

US-08-466-033-234
; Sequence 234, Application US/08466033
; Patent No. 5766840
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Wages, John
; APPLICANT: Young, Lavonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; TITLE OF INVENTION: Cloning Thereof
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466.033
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/389,886
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,509

; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,729
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,271
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,558
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,543
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,985
; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4500-0201.36/G100P11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 234:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9327 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: 3ZHEV-6, HGV FROM PNF2161
; US-08-466-033-234

Query Match 83.9%; Score 7885.6; DB 1; Length 9327;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 8433; Conservative 0; Mismatches 894; Indels 1; Gaps 1;

QY 40 GCAAGCCCCATAAACCGACGCGCTATCTAAGTAGAGCAATGACTCGGCGCCGACTCGGCG 99
Db 1 GCAAGCCCCAGAAACCGACGCGCTATCTAAGTAGAGCAATGACTCGGCGCCGACTCGGCG 60
QY 100 ACCGCCCAAAAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 159
Db 61 ACCGCCCAAAAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 120
QY 160 CCGTGTAGCCACTATAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 219
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QY 220 GAGACCGCGCAGGTCACAGGTGCTGCGCCCTACCGGTTGTAATAGGGCCCGACGTGAC 279
Db 181 GAGACCGCGCAGGTCACAGGTGCTGCGCCCTACCGGTTGTAATAGGGCCCGACGTGAC 240
QY 280 GCTCGTGTAAACCGAGCGCGCTACCCACCTGGGCAACAGCGCCAGCTAGGTGTCAC 339
Db 241 GCTCGTGTAAACCGAGCGCGCTTACCCACCTGGGCAACAGCGCCAGCTAGGTGTCAC 300
QY 340 GTCGCCCTTCAATGCTCTCTTTGACCAATAGGTTTATCCGGCGAGTTGACAGAGGACAGT 399
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QY 400 GGGGGCCGGGGGTTATGGGGAAGGACCCCAACCTTCCCGCTTCCCGGTGGCGCGGGAAT 459
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QY 460 GCATGGGCGCACCCAGCTCCGGCGGCGCTGCAGCGGGGTAGCCCAAGAAATCTTCGGG 519
Db 420 GCATGGGCGCACCCAGCTCCGGCGGCGCTGCAGCGGGGTAGCCCAAGAAATCTTCGGG 479
QY 520 TGAGGGCGGGTGGCATTTCTCTTTTCTATACCATCATGCGAGTCTCTTCTGCTCTCTTCG 579

||||| 480 TGAGGGCGGTGGCAATTTCCCTTTTCTATACCATATGGCAGTCCCTCTGCTCCTCTCG 539
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Db 540 TGGTTGAGCCGGGGCCATTCTGCCCGGCCACCCACGCTTGTTCGAGCGAATGGGCAAT 599
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QY 820 GGGCCCTTCTCGGCTCTCGGCTTACGTAGCCGGGATCCCTGGGTCTGGGGAGGTTTACTCGG 879
Db 780 GGGCCCTTCTCGGCTCTCGGCTTACGTAGCCGGGATCCCTGGGTCTGGGGAGGTTTACTCGG 839
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Db 900 GTGAGTGCCTGTGAGTTAAAGTGGGAAAGTGTGAGTGTGGAGATGGACTGAACAGTGG 959
QY 1000 CCTCAATTAAGTGTGGAATACCTTTTGGAAAGTCCCAATTTGAATTTTGGAGAGGAG 1059
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QY 1060 TGATGAGCCTGACCCCTCTGTGTGTGGTGGCCGATCTGTTTCTGCTGAGCAACCGA 1119
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QY 1300 GTGACTGCCCAACGGCCCTGGGTTTGGGTCCCGGCTTTTGGCAGCGGCTTGGGTGGG 1359
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QY 1360 GCGACCCCATCACCAATTGGAGCCACGACAAAACAGTGGGCCCTATCATGCCCCCAAT 1419
Db 1320 GTGACCCCATCACATTATGGAGCCACGGGCAAAATCAGTGGSCCCTTTTCATGCCCCCAGT 1379
QY 1420 ATGTCTATGGTCTGTGTCGTACGTGCTGTGTGGGGTTCGGTCTCTGTGTTGCCCTCGA 1479
Db 1380 ATGTCTATGGTCTGTACAGTCACTTGTGCTGTGGGGTTCGGCTTCTGTGTATGCCCTCA 1439
QY 1480 CCGGCGGTGTGATTGCAAGATCGATGTGTGAGTTTGGTCCGGTGTGGATCTGCCAGCT 1539
Db 1440 CCAAGTGTCCGACTCGAAGATAGATGTGTGAGTTTGTAGTCCAGTGTGGCTCTGCCACCT 1499
QY 1540 GCACCATAGCCGCTCTAGGGTCTATCGGATCGGACACGGTGGTTGAGCTCTCCGAGTGGG 1599
Db 1500 GCACCATAGCCGACTTGGATCATCGGATCGGACACGGTGGCTCTCCGAGTGGG 1559
QY 1600 GAGTCCCGTGGTAACTGTATTCTGACCGCTCGGCCCTGCTTATGTGGACCTGTGTGC 1659
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Db 1560 GAATCCCGCTCGTGACGCTGTGTTCTTGACCGCTCGSCCTGCTTTCATCGCGCACCTGTGTGA 1619
QY 1660 GGGACTCTGCGCCGAAACCGGGTCGGTTAGATTCCCTTTCCATTCGTTGGGACGCGGGC 1719
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Db 1740 TTAGGGGGCCCCCTGGGCAACAGGGCCGAGCAACCGGTGCGGTGCGCCCTGGGTTTTG 1799
QY 1840 GGTCTACACCATGACCAAGATCCGGGATCCCTGCAATTTGGTGAAATGTCCACACACAG 1899
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QY 1900 CCATAGAGCTTCGACTTGAACGTTTCGGGTTCCTCCCGGAGTCCCGCCCAATTAACAAC 1959
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QY 1960 GCATGCGCTTAGGACAGGAAGTGTCTGAGGATTTGGGCGGAGCTGGGCTTACGGGGGGT 2019
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QY 2020 TCTACGAGCTCTGGTTCGAGGTGTTCGAGCTGTGAGGCTGTGGGCGGAGCTTACGGGTTG 2079
Db 1980 TCTATGAACCCCTGGTGGCAGGTTTTCGAGCTGTATGGGAAGCCGAAATCCGGTTTGTG 2039
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QY 2140 TGAGAGGTTGGATGCGGGCAACTTCATCCCTCTCCACGCTGGTGTCTCTGGATTTG 2199
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QY 2200 TATTTGCTCTCTATCTATGAGCTGGCTGAGGACGCTGGTCCCGCTGATCTTGC 2259
Db 2160 TATTTGCTCTTATACCTGATGAGCTGGCTGAGGACGCTGGTCCCGCTGATCTTGC 2219
QY 2260 TTCTGCTGTGTGGTGAACCACTTGGCGGTTCTTAGGACTGCCGGCTGTGGACGCTG 2319
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Db 2280 CCGTGGCAGTGAAGTCTTCGCGGGCCCTGCCCTGTCTGCTGGGACTCCCGGCTG 2339
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QY 2440 GCCTCATGTTCTCGTGTGTGAAGCTCGCTGGGAGGCTTCCCGCTGGCATTTTGA 2499
Db 2400 GCCTGATGTTCTCGTGTGTGAAGCTTGTCTGGGAGGCTTCCCGCTGGCCCTCTTGA 2459
QY 2500 TGGGGAATTCGGGACCCCGGGCGCACCTGTGTGCTCGGGCGGAGTTCTGCTTCCATG 2559
Db 2460 TGGGGAATTCGGGACCCCGGGCGCACCTCAGTGTCTGGGGCGGAGTTCTGCTTCCATG 2519
QY 2560 TCACATTGAGGTTGACACTTCGGTGTGGGCTGGGTGGTGGCAGGCTGGTGGCTTGGG 2619
Db 2520 CTACATTGAGGTTGACACTTCGGTGTGGGCTGGGTGGTGGCAATGTGTAGCTTGGG 2579
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QY 2680 GAGTGGCTCTAAAGGTTACAGGCTGTGCGCCAGAGGTTGGTGGGAGCCCTCCGCGG 2739
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Db 9300 TGAGATCTGAAGGGGTGCACCCGGGAA 9327

RESULT 9
US-08-444-733-234
; Sequence 234, Application US/08444733
; Patent No. 5824507
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; APPLICANT: Wages, John
; APPLICANT: Young, LaVonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; TITLE OF INVENTION: Cloning Thereof
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,733
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/389,886
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/357,509
; FILING DATE: 16-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,729
; FILING DATE: 26-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,271
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/285,558
; FILING DATE: 03-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/246,985
; FILING DATE: 20-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 234:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9327 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO

; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: 3ZHV-6, HGV FROM PNF2161
US-08-444-733-234
Query Match 83.9%; Score 7885.6; DB 1; Length 9327;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 8433; Conservative 0; Mismatches 894; Indels 1; Gaps 1;
QY 40 GCAAGCCCCATAAACCCGACGCGCTATCTAAGTAGACGCAATGACTCGGCGCGGACTCGGCG 99
Db 1 GCAAGCCCCAGAAACCCGACGCGCTATCTAAGTAGACGCAATGACTCGGCGCGGACTCGGCG 60
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QY 340 GTCGCCCTTCAATGTCTCTTTGACCAATAGGTTTATCCGGCGAGTTGACAAGACCAAT 399
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QY 400 GGGGGCGGGGTTATGGGAAGCAGCCCAACCTCCCTTCCCGTGGGCGGGGAAT 459
Db 361 GGGGGCGGGGCT-TGGAGAGGAGCTCCAAGTCCCGGCTTCCCGTGGGCGGGGAAT 419
QY 460 GCATGGGGCCACCCAGCTCCCGCGCGGCTGCAGCCGGGGTAGCCCAAGATCTTCGGG 519
Db 420 GCATGGGGCCACCCAGCTCCCGCGCGGCTGCAGCCGGGGTAGCCCAAGATCTTCGGG 479
QY 520 TGAGGGGGGTGGCATTTCTTTTATACCATCATGCGAGTCCCTTCTGCTCTCTTCG 579
Db 480 TGAGGGGGGTGGCATTTCTTTTATACCATCATGCGAGTCCCTTCTGCTCTCTTCG 539
QY 580 TGGTTGAGGGCGGGCCATCTGCGCCCGGCGCCACCGCTTTCGAGCGCAATGGCAAT 639
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QY 640 ATTTCCCTCACAATTTGCTGTGCCCGGGAACATCGGGTTCTGCTTGAAGCGCGATGCC 699
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Db 720 TGGCTGTGGCCCTGGCAAGTCCCGCGCCCGGCTTGGGGAACCTGGGAGCGCTGTACG 779
QY 820 GGCCCTTGTGCGGTCTCGGCTTACCTAGCGGGATCCCTGGGCTCGGCGAGGTTTACTCCG 879
Db 780 GGCCCTTGTGCGGTCTCGGCTTACCTAGCGGGATCCCTGGGCTCGGCTGAGGTGTACTCG 839
QY 880 GGGTCTGTACAGTTGGTGTGCGTTGAGGGCGCGGGTCTACCTGATGCCAACCTGAAT 939
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QY 940 GTGCAGTAGAATGTACGTTAAGTGGGGAAGTGGATTTGGAGATGACGTAGACAGTTGG 999
Db 900 GTGCAGTCCGCGTGTGAGTTAAAGTGGGAAAGTGGATTTGGAGATGAGCTGAACAGCTGG 959

[illegible]

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Db	2100	TGCAGGAGGTGGATGCAGGCAACTTCATCCCGCCCCGCGCTGGTTCCTTTGACTTTG	2159
Qy	2200	TATTTGTCCTGCTCTATCTGATGAAGCTGGCTGAGGCACGGTTGTCCTCGTTGATCTTGC	2259
Db	2160	TATTTGTCCTGTTATACCTGATGAAGCTGGCTGAGGCACGGTTGTCCTCGCTGATCTTGC	2219
Qy	2260	TTCTGCTGTGGTGGTGAACCACTTTGGCGGTTCTTAGGACTGCCGGCTGTGAGACGCTG	2319
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Qy	2740	AGGGCGCTCTACCAAGCTTCTGACGTTCTCGCCTGGTGTGGCTTGGCCCTACATACCTGGCCG	2799
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Qy	2800	ATGCTGTGATGATGGTGGTGGCTTTGGTCTCTCTTTGCGGCTGTTCGACGCACTTGG	2859
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Qy	2860	ACTGGGCGCTGGAGGAGCTCTCGTCTCCCGGCCCTCGTTACGGGAGCTGGCAGCGGTGG	2919
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Qy	2980	CGCAAGAGGGGCCCTACCTGTTTGACCAATGGGCTCTTTCTTCGCGCGCTGTCTAAGGAGC	3039
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Qy	3040	GCTTGTGGTAAATGGGAGCGGCTTTGGAGCCCTTGTCTATCTACTAGGACGGACTCTGCCA	3099
Db	3000	GCTTGTGGTAAATGGGAGCGGCGCTTTGAACCTCTGTCTATCTACTAGGACGGACTCTGCCA	3059
Qy	3100	TCATCAGAGATGCCGCGAGGACCTGTCTTCGGGACAGTGGCTCATGGTGTTCACCGTGG	3159
Db	3060	TCATACGGGATGCCGCGAGGACTTTGTCTTCGGGGCAATGGCTCATGGGTTTACCGTGG	3119
Qy	3160	TAGCACGCGCGGTGATGAGGTTTCTCATCGGCTCTTTCAGGATGTGAATCATTTGCCTC	3219

Db 3120 TTCCGGCCGCTGGTGATGAGGTTCTCATCGGCGCTCTCCAGGATGTAATCATTTGCCCTC 3179
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Db 3180 CCGGGTTTGTTCGACCGCGCTGTGTCTATCCGACGGTCCGGAAGAGGCTTCTTGGGG 3239
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QY 3400 TCCATGGGGCTTCATCCCGAACCATCCACAGCCCGTGGGGCCCTTAATCCCGAGTGT 3459
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QY 3460 GGTACGCCAGTGATGACGTACCGGTGTACCGGTTCAGATGGGGCAACTTCGTTGACGC 3519
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QY 3700 TGTCTCACCTTGGCCGACAGGTTACTTGGCGCGGATTCCTAGTCCGCTGGACTCAAGTAC 3759
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QY 3820 AGCCCGCTGTGTTATGCTTACGGGGGCGGGAAGAGCACCCGCTACCGTTGGAGTACG 3879
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QY 3880 GCAACATGGCCACAGGCTTGTGACTTGAACCCGTCGCTAGTACCCTGAGGGCCATGG 3939
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RESULT 10
US-08-464-134-234
; Sequence 234, Application US/08464134
; Patent No. 5849532
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu P.
; APPLICANT: Wages, John
; APPLICANT: Young, LaVonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linmen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; TITLE OF INVENTION: Cloning Thereof
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

Query Match 83.9%; Score 7885.6; DB 2; Length 9327;
Best Local Similarity 90.4%; Pred. NO. 0;
Matches 8433; Conservative 0; Mismatches 894; Indels 1; Gaps 1;

Qy	40	GCAAGCCCCATAAACGACGCCCTATCTAAGTAGACGCAATGACTCGGCCCGACATCGCGC	99
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Qy	100	ACCGGCCAAAAGTGTGGTGATGGTGGTGACAGGGTGTGTAGGTGCTAATATCCCGGTCAAT	159
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Qy	160	CTGTGTAGCCACCTATAGTGGGGTCTTTAAGAGAAGGTCAAGACTCCTCTTTGTGCTGCTCGCGC	219
Db	121	CTTGGTAGCCACCTATAGTGGGGTCTTTAAGAGAAGGTTAAGATTCTCTTTGTGCTGCGCGC	180
Qy	220	GAGACGCGCACGGTCCACAGGTGTGTGGCCCTACCGGTGTGAATAAGGCGCCGACGTCTAG	279
Db	181	GAGACGCGCACGGTCCACAGGTGTGTGGCCCTACCGGTGGGAATAGGCGCCGACGTCTAG	240
Qy	280	GCTCGTGTTTAAACGAGCCGCTACCCACCTGSGGCAAAAGCGCCACGTAAGGTGCCAC	339
Db	241	GCTCGTGTTTAAACGAGCCGCTTACCCACCTGGGCAAAAGCGCCACGTAAGGTGCCAC	300
Qy	340	GTGCGCCCTTCAATGTCTCTTGTGACCAATAGGTTTATCGGGCGAGTTGACAAGGACCAAT	399

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Qy	1600	GAGTCCGCTGCGTAACTGTATCTTGGAACGCTCGGCCTGCTTCATGTGGACACTGTGTGTC	1659
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Qy	1660	GGACTGCTGGCCCGAAACCGGGTCGGTTAGATTCCCTTTCCATFCGCTGGGACACGGGCG	1719
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Qy	1960	GCATGCCGCTAGGACAGGAAGTCTCTAGAGCATTTGGCGGAGCTGGGCTTACGGGGGGGT	2019
Db	1920		
		GCATGCTTTGGGACGGAAGTGTCCGAGGCATTTGGGGGGCTGGCTCACGGGGGGT	1979
Qy	2020	TCACAGAGCTCTGGTTCCGAGTGTTCGGAGCTGATGGGACGCCGAATTCGGGTTTGC	2079
Db	1980		
		TCATGAACCCCTGGTCGCAAGTGTTCGGAGCTGATGGGAAGCCGAAATCCCGGTTGTC	2039
Qy	2080	CGGGTACGATGGCTGTCTCTGTAGACCTGACGGGTTTCATACAGCTCCAGGGGCACC	2139
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Qy	2260	TTCTGCTGTGGTGGGTGAACCAAGTTGGGGTTTCTAGGACTCCCGGCTGTGGACGCTG	2319
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QY 5620 CCGCTTCTACCTCATGCGGTTGGGCTGGAGGCAACGCGCAACCCGCTTAGCCTTCG 5679
Db 5580 CCGCTTCTACCTCATGCGGTTGGGCTGGAGGCAACGCTCAGAGCGCTGTGGCATCTG 5639
QY 5680 CTCTCTACTAGGGCGGCTGGGACGCTGTGGCAGCGCTGTGGGCTTAACCATGG 5739
Db 5640 CCCTCTCTATTTGGGGGCTGTGGAAACCGCTTGGGCACTCTCTGCTGGGCTTGACCATGG 5699
QY 5740 CGGGCGGCTTCATGGGAAGTGTAGGCTCTCCCGCTCTCTTGGTCAACATTTTACTGGGG 5799
Db 5700 CAGGTGGTTCATGGGGGCGGAGTGTCTCCCGCTCTTGGTCAACATTTTATGGGG 5759
QY 5800 CCGTGGGGGCTGGGAGGCGTGGTGAATGCGGCTAGCCTTGTCTGACTTTATGGCGG 5859
Db 5760 CCGTGGAGGTTGGGAGGTTGTGTAACGCGGCGAGCCTAGTCTTTGACTTTCATGGCGG 5819

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 234:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9327 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: 32HGV-6, HGV FROM PNF2161
US-08-461-361-234

Query Match 83.9%; Score 7885.6; DB 2; Length 9327;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 8433; Conservative 0; Mismatches 894; Indels 1; Gaps 1;
QY 40 GCAAGCCCAATAAACCGACGCTATCTAAGTACGACGCAATGACTCGCGCGGACTCGGCG 99
DB 1 GCAAGCCCAATAAACCGACGCTATCTAAGTACGACGCAATGACTCGCGCGGACTCGGCG 60
QY 100 ACCGGCCCAAAAGGTGGTGGTGTGACAGGGTGGTAGGTCGTAATCCCGGTCAT 159
DB 61 ACCGGCCCAAAAGGTGGTGGTGTGACAGGGTGGTAGGTCGTAATCCCGGTCAC 120
QY 160 CCTGGTAGCCACTATAGTGGGCTTTAAGAGAGGTCAAGACTCCTCTGTGCTCGGCG 219
DB 121 CTTGGTAGCCACTATAGTGGGCTTTAAGAGAGGTCAAGACTCCTCTGTGCTCGGCG 180
QY 220 GAGACCGCGACGCTGACAGGCTGCTGCGCTACCGCTGTAAGTAAAGGCGCGGACGTCAG 279
DB 181 GAGACCGCGACGCTGACAGGCTGCTGCGCTACCGCTGTAAGTAAAGGCGCGGACGTCAG 240
QY 280 GCTCGCTTAAACCGGACGCTGACAGGCTGCTGCGCTGTAAGTAAAGGCGCGGACGTCAG 339
DB 241 GCTCGCTTAAACCGGACGCTGACAGGCTGCTGCGCTGTAAGTAAAGGCGCGGACGTCAG 300
QY 340 GTCGCGCTTAAATGTCCTCTGACCAATAGGTTTATCCGGCGAGTTGACAAAGACCAAT 399
DB 301 GTCGCGCTTAAATGTCCTCTGACCAATAGGTTTATCCGGCGAGTTGACAAAGACCAAT 360
QY 400 GGGGCGCGGGGTTATGGGAAGGACCCCAACCTGCTCCCTTCCCGTGGGCGGGGAAT 459
DB 361 GGGGCGCGGGGTTATGGGAAGGACCCCAACCTGCTCCCTTCCCGTGGGCGGGGAAT 419
QY 460 GCATGGGGCCACCGAGCTCCCGCGGCGCTGACAGCGGGGTAGCCCAAGAAATCCTTCGGG 519
DB 420 GCATGGGGCCACCGAGCTCCCGCGGCGCTGACAGCGGGGTAGCCCAAGAAATCCTTCGGG 479
QY 520 TGAGGGGGGTGGCATTTCTTTTCTATACCATATGACAGTCCCTCTGCTCTCTTCG 579
DB 480 TGAGGGGGGTGGCATTTCTTTTCTATACCATATGACAGTCCCTCTGCTCTCTTCG 539
QY 580 TGGTTGAGCGCGGGCCATTTCTGCGCGCGGCTGACAGCGGCTGTCGAGCGCAATGGGCAAT 639
DB 540 TGGTTGAGCGCGGGCCATTTCTGCGCGCGGCTGACAGCGGCTGTCGAGCGCAATGGGCAAT 599
QY 640 ATTTCTCTACAAATTTGTTGTCGCGCGGCAATCGGCTTCTGCTGGAAGCGGATGCC 699
DB 600 ATTTCTCTACAAATTTGTTGTCGCGCGGCAATCGGCTTCTGCTGGAAGCGGATGCC 659
QY 700 TGGTGGCGCTGGGTGACAGGTTTGGACCGACCGTTCGTGGCCACTGTATCAGCGCGGTT 759
DB 660 TGGTGGCGCTGGGTGACAGGTTTGGACCGACCGTTCGTGGCCACTGTATCAGCGCGGTT 719
QY 760 TGGCTGTGCGGCTGGGAAGTCCCGCGCGGCTGCTGGGAACTGGGAGCGCTGTACG 819
DB 720 TGGCTGTGCGGCTGGGAAGTCCCGCGCGGCTGCTGGGAACTGGGAGCGCTGTACG 779
QY 820 GGGCCTTTGTCGGTCTCGGCTTACGTAGCGGGATCTCGGCTGGGCGAGGTTTACTCGG 879

DB 780 GGGCCCTGTGCGCTGCGCCTATGTGCTGGGATCTCTGGGCTGGGTGAGGTGCTACTCGG 839
QY 880 GGGTCCCTGACAGTTGGTGGTGGTGGGCGCGGCTACCTGATGCCCAACCTGAAGT 939
DB 840 GTGTCTTAACGGTGGGAGTGGGTTGACGCGCGGAGTCTACCCGGTCCCTAACCTGACGT 899
QY 940 GTGCAGTAGAATGTGACGTTAAAGTGGGAAAGTGGTGGTGGAGATGACGACGATGG 999
DB 900 GTGCAGTCGCTGTGAGTTAAAGTGGGAAAGTGGTGGAGATGACGACGATGG 959
QY 1000 CTTCCAAATTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1059
DB 960 CTTCCAAATTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1019
QY 1060 TGATGACGCTGACCCCTCTCTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1119
DB 1020 TGATAAGCCCTGACCCCTCTCTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1079
QY 1120 TTGTATGTTTCTCTGCTGCTGACGATGGCGGATGTTGCAAGGCGCGCGGCTCCG 1179
DB 1080 TTGTATGTTTCTCTGCTGCTGACGATGGCGGATGTTGCAAGGCGCGGCTCCG 1139
QY 1180 TTTTGGGTCCTCCGCTCTGCTGCTGACGATGGCGGATGTTGCAAGGCGCGGCTCCG 1239
DB 1140 TTTTGGGTCCTCCGCTCTGCTGCTGACGATGGCGGATGTTGCAAGGCGCGGCTCCG 1199
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QY 1300 GTGACTCCCGCAACGGGCTCTGCTGCTGACGATGGCGGATGTTGCAAGGCGCGGCTCCG 1359
DB 1260 GTGACTCCCGCAACGGGCTCTGCTGCTGACGATGGCGGATGTTGCAAGGCGCGGCTCCG 1319
QY 1360 GCGACCCCATCACCATTTGAGGCTGCTGCTGACGATGGCGGATGTTGCAAGGCGCGGCTCCG 1419
DB 1320 GTGACCCCATCACCATTTGAGGCTGCTGCTGACGATGGCGGATGTTGCAAGGCGCGGCTCCG 1379
QY 1420 ATGCTATAGGCTGCTGCTGCTGACGATGGCGGATGTTGCAAGGCGCGGCTCCG 1479
DB 1380 ATGCTATAGGCTGCTGCTGCTGACGATGGCGGATGTTGCAAGGCGCGGCTCCG 1439
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DB 1440 CCAGTGTGCGGCTGCAAGATAGTGTGGAGTTAGTGGAGTTAGTGGAGTTAGTGGAGTTAG 1499
QY 1540 GCACCATAGCGGCTCTAGGCTCATCGGATCGGACCGGATGGTGGTGGTGGTGGTGGTGGTGG 1599
DB 1500 GCACCATAGCGGCTCTAGGCTCATCGGATCGGACCGGATGGTGGTGGTGGTGGTGGTGGTGG 1559
QY 1600 GAGTCCCGTGGTAAAGTGTATCTGACGCTGCGGCTGCTGATGTTGCAAGGCGCGGCTCCG 1659
DB 1560 GAAATCCCGTGGTACGCTGCTGCTGACGCTGCGGCTGCTGATGTTGCAAGGCGCGGCTCCG 1619
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DB 1620 GGGACTCTGCGCGGAAACCGGCTGCTGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1679
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DB 1680 CTGCGCTGACAAAGGACTTGGAAAGTCTGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1739
QY 1780 TAAGGGGCGGCTGGGCAACCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1839
DB 1740 TAAGGGGCGGCTGGGCAACCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1799
QY 1840 GGTCTTACACATGACCAAGTCCCGGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1899
DB 1800 GGTCTTACACATGACCAAGTCCCGGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1859
QY 1900 CCATAGAGCTTCCGATGGAACGTTTCGGGTTCTTTCGGGAGTCCCGGCTTAAACACT 1959
DB 1860 CCATAGAGCTTCCGATGGAACGTTTCGGGTTCTTTCGGGAGTCCCGGCTTAAACACT 1919

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Qy 2020 TCTACGAGCCCTCTGTTCCGCAAGGTGTTCCGAGCTGTATGGGACGCGCAAAATCCGFTTCC 2079
Db 1980 TCTATGAACCCCTGGTGGCCAGGTGTTCCGAGCTGTATGGGAGCCGAATCCGGTTTGT 2039
Qy 2080 CGGGGTACGCATGCTCTCTCTGCTAGACCTGACGGGTTTATACACGTCCAGGGGCACC 2139
Db 2040 CCGGGTTTGCATGCTCTCTCTCGGCAAGCTGTATGGGTTTATACATCTCCAGGGTCACT 2099
Qy 2140 TGCAGGAGTGGATGGGGCAACTTCACTCCCTCTCCACGCTGGTTGCTCTTGGATTTG 2199
Db 2100 TGCAGGAGTGGATGGAGGCAACTTCACTCCCGCCCGCGCTGGTGTCTCTGGACTTTG 2159
Qy 2200 TATTTGCTCTCTATCTGATGAAGCTGGCTGAGGCACGGTTGGTCCGCTTGATCTTGC 2259
Db 2160 TATTTGCTCTATACCTGATGAAGCTGGCTGAGGCACGGTTGGTCCGCTGATCTTGC 2219
Qy 2260 TTCTGCTGTGGTGGGTGAACCAAGTTGGCGGTTCTAGGACTGCCGCTGTGACAGCTG 2319
Db 2220 TGCTGCTATGGTGGGTGAACCAAGCTGGCAGTCTTAGGGCTGCCGCTGTGGAAGCG 2279
Qy 2320 CCGTGGCGGTGAAGTTTTCGGGCGCTGCTTGTCTGCTGTTGGGCTTCCCACGTG 2379
Db 2280 CCGTGGCAGGTGAGGTCTTTCGGGCGCTGCTGCTGCTGTTGGGACTCCCGGTG 2339
Qy 2380 TCAGTATGATACTAGTCTAGCAAACTTGGTGTGTTGTTACTTTTCGGTGGATGGCCCTCAGC 2439
Db 2340 TCAGTATGATATGGTTTGGCAAACTTGGTGTGTTGTTACTTTAGATGGTTGGGACCCCAAC 2399
Qy 2440 GCCTCATGTTCCCTGCTGTTGGAAGCTGCTCGGGGAGCTTTCGCCGTGBCACTTTGA 2499
Db 2400 GCCTCATGTTCCCTGCTGTTGGAAGCTGCTCGGGGAGCTTTCGCCGTGBCACTTTGA 2459
Qy 2500 TGGGATTTCCGGGACCGCGGGGCACTCTGCTGCTCGGGGCGGAGTTCGCTTCGATG 2559
Db 2460 TGGGATTTCCGGGACCGCGGGGCACTCTGCTGCTCGGGGCGGAGTTCGCTTCGATG 2519
Qy 2560 TCACATTCGAGTGGACACTTCGCTGTTGGGCTGGGTTGGTGGTGGCCAGCGTGGCTTGG 2619
Db 2520 CTACATTCGAGTGGACACTTCGCTGTTGGGCTGGGTTGGTGGTGGCCAAATGTTGTTGG 2579
Qy 2620 CCATAGCCTCTGAGCTCAATGAGCCAGGCGGGGTGGAACACAAAGCCCGTGFATATA 2679
Db 2580 CCATTCGCTCTGAGCTCGATGAGCGAGGGGGTGGAGGACAAAGCCGTGATCTATA 2639
Qy 2680 GGAGTGGTGTAAAGGTACCAGGCTGTGCCAGAGGGTGTGGGAGCCCGCTCGGG 2739
Db 2640 GGAGTGGTGTAAAGGTACCAGGCAATCCGTCGAAGGGTGTGAGGAGCCCGCTCGGG 2699
Qy 2740 AGGGGCTCTTACCAAGCTTCTGCTGCTGGTGTGGGCTGGGCTTCAATCATCTGGCCGG 2799
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Qy 2800 ATGCTGATGATGTTGGTGGCTTGGTGTCTCTCTCTCGGCTGTTCGACGCACTGG 2859
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Qy 2860 ACTGGGCTTGGAGGCTCTTGTCTCCCGGCTCTGTTACGGGCACTGGCAGGGTGG 2919
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Qy 2980 GCGCAAGAGGGGCTTACCTGTTTACCACATAGGGCTCTTCTCGCGCGCTGTCAAGAGC 3039
Db 2940 GTGCGAGAGGAGCTTATTTGTTGATCATATGGGCTCATTTTCGGTGTCTCTCAAGAGC 2999

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Qy 3100 TCATCAGAGATCCCGCAGGAGCCCTGTCTCGGGAGTGGGTGATGCTGTTTACCCGTGG 3159
Db 3060 TCATACGGGATGCCCGAGGACTTTGTCTCGGGCAATGCGTCATGGTTTACCCGTGG 3119
Qy 3160 TAGCACGCGCGGTGATGAGGTTCTCATCGGCGTCTTTTTCAGATGTGAATCATTTGCCCTC 3219
Db 3120 TTGCGCGCGGTGATGAGGTTCTCATCGGCTTCTTCCAGGATGTGAATCATTTGCCCTC 3179
Qy 3220 CCGGTTTGTCCCGACTGCACAGTTGTATCCCGTGGTGGGAAGGCTTCTTGGGG 3279
Db 3180 CCGGTTTGTTCGACCGCGCTTGTGTATCCGAGGTCGGAAGGCTTCTTGGGG 3239
Qy 3280 TCAGAAAGGAGCTTACAGTGGGATCTGTACTTACATCCAGGAACTCATGTTGT 3339
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Qy 3340 TGGGACCGGCTACGTCACGAAGTGGGCACTGTCTGAATGGGCTGTGTTTCAAACTT 3399
Db 3300 TGGGACCGGCTACGTCGGAAGTGGGCACTGTCTGAATGGGCTGTGTTTCAAACTT 3359
Qy 3400 TCCATGGGCTTCACTCCGAACCATCGCCCGTGGGCGCTTAAATCCAGGTTGT 3459
Db 3360 TCCATGGGCTTCACTCCGAACCATCGCCCGTGGGCGCTTAAATCCAGGTTGT 3419
Qy 3460 GGTACGCGAGTGTACGCTACGGTGTACCGCTTTCAGATGGGGCACTTCGTTGAGCG 3519
Db 3420 GGTACGCGAGTGTATGATGTACGGTGTATCCACTCCCGGATGGGCTACTTCGTTAAGCG 3479
Qy 3520 CCGTACATTCGCGAGCGGAGTCTGTTGGTATTTAGATTCGACGGGCTTGTGTCATG 3579
Db 3480 CTTGTACTTTCGAGGCTGAGTCTGTTGGTGTATCAGATCCGACGGGCGCTATGCCATG 3539
Qy 3580 GCTTGAGCAAGGGGAGCAAGTGTGAGCTGGATGGCCATGAGGCTCTGACTTCCGCTG 3639
Db 3540 GCTTGAGCAAGGGGAGCAAGTGTGAGCTGGATGGCCATGAGGCTCTGACTTCCGCTG 3599
Qy 3640 GTTCGCTGGTTACCGGCTCTTTCGCAAAAGGCGACGAGTAAAGATGCTCGTGCAG 3699
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Qy 3700 TGCTCCACTCTGGCGGAGGGTGTACTGGGCGGATTTCACTAGGCGGTGGACTCAAGTAC 3759
Db 3660 TGCTTCACTCCGGTGTAGGTCACCGGCGCACGGTTTCACTAGGCGGTGGACCCAAGTGC 3719
Qy 3760 CAACAGATGCCAAAGTACCACAGAAACCCCTTCGGGTGCGGCAAAAGAGTTCACAAAG 3819
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Qy 3820 AGGCGCGCTTGTATGCTACGGGGCGGGAAGAGCACCGCGTACCGTTGGAGTACG 3879
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Qy 6340 TTTTGAATGGCACTCAAGATCCAGTTTACTCTACCAAGCTGTGCGAGCAATTATGA 6399
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Qy 6820 CGGCTGACCCCTTCAGGCTATCGAGAAATGCTGCGGAGAAATCTTGAACCTCATATAGTG 6879
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Qy 6880 TCATCATGAAGATTCAGTACACCTCTCTTGTGGAGTAGCCGAGAGAGCTCTGCT 6939
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Qy 6940 GGGGGAAGACATACCCCGACTTCCATCGCCAGCACTTATCTCGGTTACTGAGAGCAGCC 6999
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Qy 7180 TGTCTGCTGTGTGAGAAGAGCGTAACACGCTCTCTTTCATTGGGATTGACGGTCGCTG 7239
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Qy 7420 CACTGACGAGGGCCACTCCGGCCAAAGCCCTGCTGCTGAGGCGGTTGCTCCTTCTGCTG 7479
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Qy 7900 TGGGAGACCTTGACGGGTAGCCAAAGCGGTGTTGGGGGGGCGCTAGCCTTCCAGTACA 7959
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Qy 7960 CCCCNAATCAGCGAATTTAGGAGATGCTCAAACTGTGGGAATCAAAAGAACACCATGCG 8019
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Db 7980 CCATCTGTGTGGACGCCACATGCTTCACAGTAGCATAACTGAAGAGAGCTGGCTTGG 8039
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Qy 8200 GATCCTCAGGGGTCTTGACACCAAGTCCAGCAACTGCTTGAATGCTATATCAAGTGA 8259
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Qy	220	GAGACCGGCACGGTCCACAGGTGCTGCGCCCTACCGGTGTAATAAGGGCCCGACGCTCAG	279
Db	181	GAGACCGGCACGGTCCACAGGTGTTGGCCCTACCGGTGGGAATAAGGGCCCGACGCTCAG	240
	280	GCTCGTCTTAAACGAGCGCGTCACCCACCTGGGCAACAGCAGCCACGTAACGGTCCAC	339
Db	241	GCTCGTCTTAAACGAGCGCGTTACCCACCTGGGCAACAGCAGCCACGTAACGGTCCAC	300
Qy	340	GTGCCCTTCAATGTCTCTTTGACCAATAGTATTATCCGGCAGGTTGACAAGGACCAAGT	399
Db	301	GTGCCCTTCAATGTCTCTTTGACCAATAGCGTAGCGGGGAGTTTGACAAGGACCAAGT	360
Qy	400	GGGGCCGGGGTATTGGGAAGGACCCCAACCCCTGCCCTTCCGGTGGCCCGGGAAAT	459
Db	361	GGGGCCGGGGGT-TGGAGAGGAGTCCCAAGTCCCGCCCTTCCGGTGGCCCGGGAAAT	419
Qy	460	GCATGGGCCACCCAGCTCCGGGGGGCTGCAGCGGGGTAGCCCAAGAAATCCTTCGGG	519
Db	420	GCATGGGCCACCCAGCTCCGGGGGGCTGCAGCGGGGTAGCCCAAGAAATCCTTCGGG	479
Qy	520	TGAGGGCGGTGGCATTTCTTTTCTATACCATCATGGCAGTCCCTTCGTCTCTTCG	579
Db	480	TGAGGGCGGTGGCATTTCTTTTCTATACCATCATGGCAGTCCCTTCGTCTCTTCG	539
Qy	580	TGTTGAGGCCGGGGCATTTGCCCCCGGCCACCCAGCTTGTGCGAGCGAATGGGCAAT	639
Db	540	TGTTGAGGCCGGGGCATTTGCCCCCGGCCACCCAGCTTGTGCGAGCAATGGGCAAT	599
Qy	640	ATTTTCCTACAAATGCTGTGCCCGGGAAGACATCGGGTCTGCTCGAAGCGGATGCC	699
Db	600	ATTTTCCTACAAATGTTGTGCCCGGAGGACATCGGGTCTGCTCGAGGGTGGATGCC	659
Qy	700	TGTTGGCCCTGGGGTGCACGGTTTGACGACGACCGTTGCTGGCCACTGTATCAGCGGGTT	759
Db	660	TGTTGGCCCTGGGGTGCACGATTTGCACTGACCAATGCTGGCCACTGTATCAGCGGGTT	719
Qy	760	TGGCTGTGGCCCTGGCAAGTCCGGGGCCCCAGCTCGTTGGGGAACTGGGGAGCCTGTACG	819
Db	720	TGGCTGTGGCCCTGGCAAGTCCGGGGCCCCAGCTGGTGGGGAGCTGGGTAGCCCTATACG	779
Qy	820	GGCCCTTGTCCGCTCCGGGTTACGTAGCCGGGATCCTGGGTCTGGCGCAGGTTTACTCCG	879
Db	780	GGCCCTTGTCCGCTCCGGCTATGTGGCTGGGATCCTGGGCTGGGTAGGTGTACTCGG	839
Qy	880	GGTCTCGACAGTTGGTGTGGGTTGAGCGCCGGGTCTACCTGATGCCCAACTGAAGT	939
Db	840	GTGTCTTAAACGGTGGGAGTCCGGTTGACGCGCGGATCTACCCGGTGCCTTAACCTGACGT	899
Qy	940	GTGCAGTAGAATGTGACGTTAAGTGGGGAAGTGAGTTTGGAGATGGACTGAGCAGTTGG	999
Db	900	GTGCAGTCCGCTGTGAGTTAAGTGGGAAGTGAGTTTGGAGATGGACTGAACAGCTGG	959
Qy	1000	CCTCCAAATTAAGTATTTTGGAAATACCTTTGGAAAGTCCCATTTGAAATTTGGAGAGGAG	1059
Db	960	CCTCCAACTACTGGAATTCGGAATACCTCTGGAAGTCCCATTTGATTTCTGGAGAGCG	1019
Qy	1060	TGATGAGCCTGACCCCTCTGTGTGGTGGGTGGCCGCAATGCTTTGCTGGAGCAACGGA	1119
Db	1020	TGATAAGCCCTGACCCCTCTGTGTGGTGGGTGGCCGCAATGCTTTGCTGGAGCAACGGA	1079
Qy	1120	TTGTGATGTTTTCGCTGGTGACATGGCGGGATGTGCAAGGCGCCCCCGCTCCG	1179
Db	1080	TTGTGATGTTTTCGCTGGTGACATGGCGGGATGTGCAAGGCGCCCCCGCTCCGCTCCG	1139
Qy	1180	TTTTGGGGTCCCGCCCTTTTGACTACGGGTTGAAAGTGGCAGTCTATGCTCTCGAGGGCTA	1239
Db	1140	TTTTGGGGTCAACCCCTTTTGACTACGGGTTGACTTTGGCAGACCTGCTTTGCGAGGCCA	1199
Qy	1240	ACGGGTCCGCTATTCCCACTGGGGAGAGGGTGTGGGATCGAGGGAATGTACGCTCTGT	1299
Db	1200	ACGGGTCCGCTTTTTCGACTGGGAGAGGGTGTGGGACCGTGGGAACCGTATGACTTCAG	1259

QY	1300	GTGACTGCCCCAAACGGCCCTCTGGGTTTGGGTCCCGGCCCTTTTGGCCAGCGGGTTGGTGGG	1359
DB	1260	GTGACTGCCCTTAACGGCCCTTGGGTGTGGTGTGCGAGCCCTTTTGGCAAGCAATCGGCTGGG	1319
QY	1360	CGGACCCCATCACCACTTGTGAGCCACGGACAAACACAGTGGCCCTATCATGTCGCCCAAT	1419
DB	1320	GTGACCCCATCACCTATTGTGAGCCACGGGCAAAATCAGTGGGCCCTTTCATGCCCCCAGT	1379
QY	1420	ATGTCTATGGGTCTGTCTCCGTAACTGTGGTGTGGGGTTCCGTGTCTTGGTTTGGCTTCGA	1479
DB	1380	ATGTCTATGGGTCTGTCTACAGTCACTTCGCTGTGGGTTCGCGTTCCTGGTATGCCCTCA	1439
QY	1480	CCGGGGTCTGTGATTCGAAGATCGATGTGTGGAGTTTGGTGTCCGGTGTGGATCTGCCAGCT	1539
DB	1440	CCAGTGGTCCGCACTCCGAAGATAGATGTGTGGAGTTTGTAGTGGCCAGTTGGCTCTGCCACT	1499
QY	1540	GCACCATAGCCGCTCTAGGGTCTATCGGATCGGCACACGTGGTTGAGCTCTCCGAGTGGG	1599
DB	1500	GCACCATAGCCGCACTTGGATCATCGGATCGGCACACGTGGCTGGGCTCTCCGAGTGGG	1559
QY	1600	GAGTCCCGTGGTAACGTGTATTCTTGGACCGTGGCGTCTCTTCATGTGCGACCTGTGTGC	1659
DB	1560	GAATCCCGTGGTGAAGCTGTGTCTTGGACCGTGGCGTCTCTTCATGTGCGCACCTGTGTGA	1619
QY	1660	GGGACTGTGTGCCCGAAACCGGCTGGTTAGATTCCCTTTCCATCGGTGCGGCACGGGGC	1719
DB	1620	GGGACTGTGCCCGGAGACCGGCTGGTTAGGTTCCCATTCCTCATCGGTGCGGCTGGGGC	1679
QY	1720	CTCGGCTGCAAAAGCACTTGGAGCTGTGGCTTGTCTCAACAGGACAACCTCCCTTTCACCA	1779
DB	1680	CTCGGCTGCAAAAGCACTTGGAGCTGTGGCTTGTCTCAATAGGACAACCTCCCTTTCACCA	1739
QY	1780	TAAAGGCGCCCTGGGCAACACGGGAGAGGCAACCGGTGCGGTGCGCCCTGGGTTTGG	1839
DB	1740	TTAAGGCGCCCTGGGCAACACGGGCGGAGCAACCGGTGCGGTGCGCCCTGGGTTTGG	1799
QY	1840	GGTCTCTACCATGACCAAGATCCGGGATTCCTCGATTTGGTGTGAATGTCCCCACACAG	1899
DB	1800	GGTCTACGCCATGACCAAGATCCGAGATACCTACATCTGTTGGAGTGTCCCACACAG	1859
QY	1900	CCATAGACCTCCGACTGGAAAGTTTGGGTTCTTCCCGGAGTCCCGGCCATTTACAACCT	1959
DB	1860	CCATCGAGCTTCCACCGGACGTTTGGGTTCTTCCCGGAGCGCGCTCTCTCAACAACCT	1919
QY	1960	CGATGCCGCTAGGCACGGAAGTGTCTGAGGCATTGGGCGGAGCTGGCTTACGGGGGGT	2019
DB	1920	GCATGCTCTTGGGCACCGGAAGTGTCCGAGGCATTTGGGGGGGCTGGCTTACGGGGGGT	1979
QY	2020	TCTACGACCTCTGGTTTCGCAAGTGTTCGGAGCTGATGGGACGCGGAATCCGGTTTGGC	2079
DB	1980	TCTATGAACCCCTGCTCCGCAAGTGTTCGGAGCTGATGGAGCGGAATCCGGTTTGTCT	2039
QY	2080	CGGGGTAGCAATGCTGTCTCTGTGTAGACCTGTACGGGTTTCATACACGTTCGAGGGCAC	2139
DB	2040	CGGGGTTTGCATGCTCTCTTTCGGGACAGGCTGATGGGTTTATACATGTCCAGGGTCACT	2099
QY	2140	TGCAGGAGTGGATGCGGCAACTTCATCCCTCCACGCTGGTTGCTCTTGGATTTTG	2199
DB	2100	TGCAGGAGTGGATGCGGCAACTTCATCCCGCCCCCGGCTGGTTGCTCTTGGACTTTTG	2159
QY	2200	TATTGTCTCTCTATCTGATGAAGCTGGCTGAGGCACGGTTGGTCCCGTTGATCTTGC	2259
DB	2160	TATTGTCTCTTATACCTGATGAAGCTGGCTGAGGCACGGTTGGTCCCGCTGATCTTGC	2219
QY	2260	TTCTGCTGTGGTGGGTGAACCAAGTTGGCGGTTCTTAGGACTGCGCGGCTGTGTGACGGTG	2319
DB	2220	TGCTGCTATGGTGGGTGAACCAAGCTGGCACTCTAGGGCTCTAGGGCTGCGCGGCTGTGGAAGCG	2279
QY	2320	CCGTGGCGGTGAAGTTTTCGCGGCCCTTCCTGTGTCATGTGTTTGGGCTCTCCCACTG	2379
DB	2280	CCGTGGCAGGTGAGGCTCTTCGCGGGCCCTTCGCCCTGTCTTGGTGTCTTGGACTTCCCGTGC	2339
QY	2380	TCAGTATGATACTAGGTCTAGCAAAACCTGGTGTGTGACTTTTCGGTGGATGGCGCCTCAGC	2439

[illegible]

Qy 8980 CCCCCTATATGGGGTGTTCATCAATGGATTTTCAAGCCAGAGGAGTGCCTGGCGGT 9039
Db 8940 CCCCCTATATGGGGTGTACACCAATGGATTTTACAGCCAGAGGAGTGCCTGGCGGT 8999
Qy 9040 GGTGGGGTCTTAGCCCTGCTCATCGTAGCCCTCTTCCGGGTGAACCTAAATTCATCTGT 9099
Db 9000 GGTGGGGTCTTAGCCCTGCTCATCGTAGCCCTCTTCCGGGTGAACCTAAATTCATCTGT 9059
Qy 9100 GCGCAAGTCCGGTGAATCATCATCTGAGAGGTTTCCCGCCCTCCCGCCCGCCAGGG 9159
Db 9060 GCGCGAGGCTGTGGTGAATCATCATCTGAGAGGTTTCCCGCCCTCCCGCCCGCCAGGG 9119
Qy 9160 GTCCTCCCGCTGGGTAAAAAGGCGCCGCTTGGGAGGCTGGTGGTAAACCCCGCTG 9219
Db 9120 GTCCTCCCGCTGGGTAAAAAGGCGCCGCTTGGGAGGCTGGTGGTAAACCCCGCTG 9179
Qy 9220 GCAGGGTCAAGCCGTGATGGTCTAATGCACTGCCACTTCGGTGGCGGGTGCCTACCTTA 9279
Db 9180 GCAGGGTAAAGCCCTGATGGTCTAATGCACTGCCACTTCGGTGGCGGGTGCCTACCTTA 9239
Qy 9280 TAGCGTAATCGTGACTACGGGCTGCTGCGAGAGCCCTCCCGGATGGGGGCACAGTGCAC 9339
Db 9240 TAGCGTAATCGTGACTACGGGCTGCTGCGAGAGCCCTCCCGGATGGGGGCACAGTGCAC 9299
Qy 9340 TGTGATCTGAAGGGGTGCACCCCGGTAA 9367
Db 9300 TGAGATCTGAAGGGGTGCACCCCGGAA 9327

RESULT 13

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; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; TITLE OF INVENTION: Cloning Thereof
; NUMBER OF SEQUENCES: 277
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; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
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Best Local Similarity 90.8%; Pred. No. 0;
Matches 8264; Conservative 0; Mismatches 839; Indels 0; Gaps 0;

Qy 76 CAATGACTCGGCGGCGACTCGGCGACCGGCAAAAGGTGGTGGATGGGTGATGACAGGCT 135
Db 1 CAATGACTCGGCGGCGACTCGGCGACCGGCAAAAGGTGGTGGATGGGTGATGACAGGCT 60
Qy 136 TGGTAGGTCGTAAATCCCGGTCATCTGTAGCCACTATAGTGGGTCTTAAGAGAAGGT 195
Db 61 TGGTAGGTCGTAAATCCCGGTCATCTGTAGCCACTATAGTGGGTCTTAAGAGAAGGT 120
Qy 196 CAAGACTCCTCTTGTGCTGGCGGAGACCGCGACCGTCCACAGGTGCTGGCCCTACCG 255
Db 121 TAAGATTCTCTTGTGCTGGCGGAGACCGCGACCGTCCACAGGTGCTGGCCCTACCG 180
Qy 256 GTGTGAATAAGGGCCCGACGTCAGGCTCGTGTAAACCGAGCCCGTCAACCCACCTGGGC 315
Db 181 GTGGGAATAAGGGCCCGACGTCAGGCTCGTGTAAACCGAGCCCGTCAACCCACCTGGGC 240
Qy 316 AAACGACCCCGACGTCACGTCACGTCGCCCTTCAATCTCTCTTGAACCAATAGGTTTA 375
Db 241 AAACGACCCCGACGTCACGTCACGTCGCCCTTCAATCTCTCTTGAACCAATAGGCTTA 300
Qy 376 TCCGCGAGTTGACAAGGACCAAGTGGGGCGGGGTTTATGGGAAGGACCCCAACCCCT 435
Db 301 GCGGCGAGTTGACAAGGACCAAGTGGGGCGGGGTTTATGGGAAGGACCCCAACCCCT 360
Qy 436 GCCCTTCCCGTGGGCGCGGAAATGATGGGCGCAACCCAGCTCCCGGGCGGCTCGACGC 495
Db 361 GCCCTTCCCGGCGGACCGGAAATGATGGGCGCAACCCAGCTCCCGGGCGGCTCGACGC 420
Qy 496 GGGGTAGCCCAAGATCTCTGGGTGAGGGGGGTGGCATTTCTCTTTCTATACCATCA 555
Db 421 GGGGTAGCCCAAGATCTCTGGGTGAGGGGGGTGGCATTTCTCTTTCTATACCATCA 480
Qy 556 TGGGAGTCTTCT 615
Db 481 TGGGAGTCTTCT 540
Qy 616 ACGCTTGTGAGCGGAATGGCAATATTTCTCACAATTTGTGTGCTCCCGGGAAGATCG 675
Db 541 ACGCTTGTGAGCGGAATGGCAATATTTCTCACAATTTGTGTGCTCCCGGGAAGATCG 600

Db	2761	 TCTTTGGCCCTGTTTCGACGCGTTTGGAGTGGGCTTTTGGAGAGAGCTCTTGGTGTGCCGGCCCT	2820
Qy	2896	CGTTACGGCGACTGCGACGGGTGGTGTAGTGTCTGTATGGCGGGCGAGAGGCCACCA	2955
Db	2821	CGTTACGGCGCTTGGCCCGGGTGGTGTAGTGTCTGTATGGCGGGGAGAGGCCACAA	2880
Qy	2956	CCATCCGACTGTGCTCCAAAGATGTGCGCAAGAGGGGCCCTACTGTTTGAACACATGGGCT	3015
Db	2881	CCGTTCGGCTGGTCTCCAAAGATGTGCGGAGAGGGCCCTATTGTTTGAACCATATGGCT	2940
Qy	3016	CTTTCTCGCGCGCTGTCAAGGAGCGCTTGTTCGAATGGGACGCGGCTTTGGAGCCCTTGT	3075
Db	2941	CTTTTTCGCGCGCTGTCAAGAGAGCGCTGCTGGAGTGGGACGCGGCTTTTGAACCCCTGT	3000
Qy	3076	CATTCACTAGGACGGACTGTGCGCATCATCAGAGATGCCCGGAGGACCGCTGTCTCGCGGAC	3135
Db	3001	CATTCACTAGGACGGACTGTGCGCATCATTTAGAGATGCTTCGAGGAGCCCTTGGCCTTCGCGGC	3060
Qy	3136	ATGTCGCTCATGGGTTTACCCTGGTGTAGCACGCGCGGGTGTATGAGGTTCATATCGGCGTCT	3195
Db	3061	AGTCGCTCATGGGCTTGGCTGTGGTAGCGCGCGCTGTGTACGAGGTTCTTATCGGTGTCT	3120
Qy	3196	TTCAGGATGTGAATCATTTTGCCTCCCGGGTTGTCCCGACTTGCACCAAGTGTGTATCCGTC	3255
Db	3121	TTCAGGATGTGAACCAATTTGCCTCCCGAATTCGTCCCGACCGCACCCGTTGTCTATCCGGC	3180
Qy	3256	GGTTCGGAAGAGGCTTTCCTGGGGGTTCACGAAGCAGCCCTTGACAGGTAGGATCCTCGACT	3315
Db	3181	GGTCGGAAGAGGGTTCCTGGGGGTCACTAAGGCTGCCCTGACTGTGGTGGGATCCTGACT	3240
Qy	3316	TATATCCAGGGAACGTATGGTGTGGGACGGCTACGTACGAAGCATGGGCACATGTC	3375
Db	3241	TATATCCAGGGAACGTATGGTGTGGGACGGCTACGTGCGGAAGCATGGGACATGCC	3300
Qy	3376	TGAATGGCCTGCTGTTCACAACATTTCCATGGGGCTTCATCCGGAACCATCGCCACGCCCG	3435
Db	3301	TGAACGGCCTGCTGTTCACGACATTTCCATGGGGCTTCATCCCGAACCATTCGCCACGCCCG	3360
Qy	3436	TGGGGGCCCTTAATCCACAGGTGTGTGTACGCCAGTGATGAGTACAGGTGTACCCGCTTC	3495
Db	3361	TGGGGGCCCTTAATCCACAGGTGTGTGTCCGCAGTGATGAGTACAGGTGTACCCGCTTC	3420
Qy	3496	CAGATGGGCAACTTCGTTGAGCCCTCGACATTGCCAGCGGAGTCTCTTGGGTATTATTA	3555
Db	3421	CGATGGGCAACCTCGTTGACGCCCTGCACATTGCCAGGCTGAGTTCCTGTGGGTATATC	3480
Qy	3556	GATCCGAGCGGGCTTTGTGCCATGGCTGTAGCAAGGGGACAAGGTTGAGTGTGATGTGG	3615
Db	3481	GGTCCACAGGGGCTTTGTGCCATGGCTTGAGTAAAGGGAGACAAGGTGAGGTAGATGTGG	3540
Qy	3616	CCATGGAGTCTCTGACTTCCGTCCGTTCGTCTGGTTTACCGGTCTTTCGACACAAGGC	3675
Db	3541	CCATGGAGTCTCTCAGATTTCCGTTCGTTCGTCCGGCTTCACCTGTCTGTGTCACGAGGGGC	3600
Qy	3676	ACGCACTAAGAAATGCTCTGCTCAGTCTCCACTCTGGCGGACAGGTTACTCTCGCGCGCAT	3735
Db	3601	ACGCACTAAGAAATGCTCTGCTCGGTCTCCACTCTCGGTTGGTTCAGCCGCGCTCGAT	3660
Qy	3736	TCACTAGCGCGTGGATCAAGTACCAACAGATGTCCAAGACTTACCACAGAACCCCTCCGG	3795
Db	3661	TCACCAAGCGCTGGACCCAGTCCCAACAGATGCTTAAGACACCACTGAACCCCTCCGG	3720
Qy	3796	TGCCGCAAAAGAGTTTTCAGGAGGGCCCCGTGTTTATGCTTACGGGGCGGGAAGA	3855
Db	3721	TGCCGCAAAAGGAGTTTTCAGGAAAGCCCCACTGTTTATGCCACAGCGGCGACGGAAGA	3780
Qy	3856	GCACCCGCTTACCGTTGGAGTAGCGGCAACATGGGCCACAAGTCTTGATCTTTGAACCGT	3915
Db	3781	GCACCGCGCTCCGTTGGAGTATGGCAACATGGGCCACAAGTCTGATTTTGAACCCCT	3840
Qy	3916	CGGTAGCTACCGTAGGGGCCATGGGCCCATACATGGAGCGGCTGGCGGGGAACACCCCA	3975

Db	3841	CGTGGCGACAGTGAAGGCCATGGGCCCTTACATGAGAGCGACTGCGGGGAAAAATCCAA	3900
Qy	3976	GTATTTACTGTGGCCATGACACCACTGCTTTTACAAAGATCACTCACTCGCCCTTACGT	4035
Db	3901	GTATCTACTGTGGCCATGACACCACTGCTTTACAAAGATCACTGATTTCCCCCTTAAGT	3960
Qy	4036	ATTCCACTTACGGAAGGTTTTTGGCCAAACCCCTAGGCAGATGCTGAGGGGTGTGCGTGG	4095
Db	3961	ACTCTACTATGGGAGGTTTTTGGCCAAACCCCTAGGCAGATGCTGCGAGGTGTGTCGGTGG	4020
Qy	4096	TCATTTGTGACGAGTCCCACAGTCATGACTCAACTGCTGTGTTGGGCATTTGGCGGTGTCA	4155
Db	4021	TCATTTGGCATGAATGCCACAGTCATGATTCACATGTGTTGTTGGGATTTGGACGGGTCC	4080
Qy	4156	GGGAGCTGGCGGAGGATGTGGAGTGCAATTTGGTGTCTTACGCCACTGCCACCCCTCCCG	4215
Db	4081	GGGAGCTGGCACGAGAGTGTGGGTGCACTTGTCTCTACGCCACTGCCACGCTCCTG	4140
Qy	4216	GATCCCGATGACCCAGACCCCATCAATCATTTGAGACAAAACTGGACGTGGGAGAGATCC	4275
Db	4141	GGTCCCCCATGACTCAGCATCCCTCAATCATTTGAGACAAATTTGATGTGGGTGAGATTTC	4200
Qy	4276	CTTTCTATGGSCATGGCATACCTCTTTGAGCGGATGGGACGGGAAGGATCTCGTATTCT	4335
Db	4201	CTTTCTATGGSCATGGCATACCCCTCGAGCGATGGGACCGGTAGGCACCTCGTATTCT	4260
Qy	4336	GCCACTCAAGGGTGAAGTCGAGCGCTGGCGGGCCAGTTTTCGGCTAGGGGGTAAATG	4395
Db	4261	GCTACTTAAGGCAGAGTGTGACCGCTAGCCGGTCAGTTTCTGCTAGGGGAGTTAAGC	4320
Qy	4396	CCATCGCCTATTACGGGGGAAAGACAGTTCTATCATCAAAGATGGAGACCTGTGTGTGT	4455
Db	4321	CCATAGCCTATTACAGGGGAAAAGACAGTTCTATCATCAAGGACGGAGATCTGTGTGTGT	4380
Qy	4456	GTGCTACAGACGCACATCACCTGGGTACACTGGGNACTTTCATTCTGTCAACCATTTGTG	4515
Db	4381	CGCGACCGACGGCCTATCCACTGSGATACACTGGGAACTTCGATTCTGTCAACCACTGTG	4440
Qy	4516	GTTTGTGTGGTGGAGAGTGTGTCGAGGTGACCTTTGATCCCAACCATTACCATCTCCCTGC	4575
Db	4441	GTTTGTGTGGTGGAGAGTGTGTCGAGGTGACCTTTGATCCCAACCATTACCATCTCCCTGC	4500
Qy	4576	GCACGGTCCCGCTGGCTGAACTGTGATGCAGCGGAGGACGCACGGGTAGGGGCA	4635
Db	4501	GGACAGTGCCCGCTGGCAGAACTGTGATGCAGAGACGAGGACGCACGGGTAGAGCA	4560
Qy	4636	GGTCTGGCGGTACTACTACGCGGGGGTGGCAAGGCCCTCTGCTGTGTGTGCGCTCAG	4695
Db	4561	GGTCTGGCGGTACTACTACGCGGGGGTGGCAAGGCCCTCTGCTGTGTGTGCGCTCAG	4620
Qy	4696	GTCCTGTCTGTGGCGGTGGAAAGCGGTGTGACCTGTGACGAATGGAACCTGACCTGA	4755
Db	4621	GTCCTGTCTGTGGCGGTGGAGCCGGAGTGACCTGTGTGGAATGGAACCTGACCTGA	4680
Qy	4756	CAGCAAACTACTGAGACTTTACGCAACTGGCCCTTACACCGCAGCCGCTCGCAGCTGACA	4815
Db	4681	CAGCTAACCTATTGAGACTTTACGACGACTGCCCTTACACCGCAGCCGCTCGCAGCTGACA	4740
Qy	4816	TTGGGGAAGCGCGGTGTTCTTTTCGGGGTGTGCCCCGTTGAGGATGATCCCGATGTTA	4875
Db	4741	TCGGTGAAGCGCGGTGTTTTCCTCCGGGTGCGAAAGGCCCTCCGCGGTGTGTGCGCTCGG	4800
Qy	4876	GCTGGCAAAAGTTCGCGGGTCAACTGCCCCCTCTCTGTGTGGTGTTCAGCGGACCATGT	4935
Db	4801	GCTGGCAAAAGTTCGCGGGTCAACTGCCCCCTCTTGTGTGGTGTTCAGCGGACCATGT	4860
Qy	4936	GCCGGGAAACACTGCTCCCGGCCCATCGGATGACCCCACTGGCGAGGTCTGAAGGCC	4995
Db	4861	GCCGGGAAACACTGCTCCCGGCCCATCGGACGACCCCACTGGCGAGGTCTGAAGGCC	4920
Qy	4996	CGAATCTGTCCCACCTCTGCTGAGGTGGGCAATGATTTACCATCTAAAGTGGCGCGCC	5055
Db	4921	CGAATCTGTTCACACTCTCTCAGGTGGGCAATGATTTACCATCAAAAGTGGCGCGCC	4980

Db 7141 TTTCTTTGGGGTGACGGTGGCTGTGTGTGGCCAGCTGTGTGAGATGGAGATCCAGAAC 7200
Qy ATACAGCCTATTGTGACAGAGTGGCCAGCTCCGCTTGAATTGACAGTGTGGTCTTGGTGG 7335
Db ATACAGCCTATTGTGACAGAGTGGCCAGCTCCGCTTGAATTGACAGTGTGGTCTTGGTGG 7260
Qy GCAATGAACCTTACCCTTTGAATGTGACAAAGTGTAGGCTAGGCAAGAGACCTTTGGCTTCC 7395
Db GCAATGAACCTTACCCTTTGAATGTGATAAGTGTAGGCTAGGCAAGAGACTTTGGCTTCC 7320
Qy TCTCTTACATTTGGTGTGGGTGACATGACAGAGGCGCACTCCGCGCAAGCCCTCTGAGG 7455
Db TCTCTTACATTTGGTGTGGGTGACATGACATGAGGCGCACTAGGCTAGGCGCAAGCCCTCT 7380
Qy TGAGGCGGTGGCTTCCCTTGTGTGGTGGCGCACACCAAGAGTGTATGTCACCAACCCGG 7515
Db TGAGGCGGTGGGTGGCTTGTGTGGTGGCGCACACCAAGAGTGTATGTCACCAACCCGG 7440
Qy ACAATGTTGGGAGAGTGTGACAAAGTGTACCTTCTGGCGTGGCCCTAGGCTTCAATGACA 7575
Db ACAATGTTGGGAGAGTGTGACAAAGTGTACCTTCTGGCGCGCCCGCCAGGCTCCATGACA 7500
Qy AATTCCTGTGACCTTCCATGAGCGGCTAAGAGGCGAGCTCAAGCCCTGCGCTTAAGCATGG 7635
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Qy GTTACATATGAGGAGCAATAAGGACTGTAAAGGCGACATGCTGCCATGGGCTGGGAT 7695
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Qy CTAAGTGTGCGTCAAGGACCTCGCCACCCCTGCGGGAAGATGCTGTCCATGACCGGC 7680
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Qy TCTCTCAAGACCGAAGGAGAGAGGCGCCCGCTCTATGTGTCTCCCGCTGGACT 7875
Db TCTCTCAAGACCGAAGGAGAGAGGCGCCCGCTCTATGTGTCTCCCGCTGGACT 7875
Qy TCTCTCAAGACCGAAGGAGAGAGGCGCCCGCTCTATGTGTCTCCCGCTGGACT 7800
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Qy TCCGGATAGCTGAAAAGCTTATCTCTGGGAGACCTGAGCGGTAGCGAGGCGGTGG 7860
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Db GGGATCAAGAGACACCATCGCCATCTGTGTGAGCGCCACATGCTTCGACAGTAGCA 7980
Qy TAACTGAAGAGACCTGCGCTGGAGACAGAGCTTTATGCGCTTCCAGACCATCAG 8115
Db TAACTGAAGAGACCTGCGCTGGAGACAGAGCTTTATGCGCTTCCAGACCATCAG 8115
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Qy AATGGTGGTGGTGGGGAATATGATGCTCTGGGCAAGTGTGAGCAAGTGAACCCCGAGGGG 8175
Db AATGGTGGTGGTGGGGAATATGATGCTCTGGGCAAGTGTGAGCAAGTGAACCCCGAGGGG 8175
Qy AGTGGTGGGAGCTTTGGGGAAGTACTATGCTCAGGAACCATGCTCAGCCCTGAGGGG 8100
Qy TGCCAGTGGTGGGAGTATGATGATCTCAGAGGCTTGGACCAAGTGGGAGCACT 8235
Db TGCCAGTGGTGGGAGTATGATGATCTCAGAGGCTTGGACCAAGTGGGAGCACT 8160
Qy GCTTACCTTGTATCAAGGTGAAGCGCTGTGAGAGGCTGGGCTGAAAAATGTCT 8295
Db GCTTACCTTGTATCAAGGTGAAGCGCTGTGAGAGGCTGGGCTGAAAAATGTCT 8295
Qy GCTTACCTTGTATCAAGGTGAAGCGCTGTGAGAGGCTGGGCTGAAAAATGTCT 8220
Db GCTTACCTTGTATCAAGGTGAAGCGCTGTGAGAGGCTGGGCTGAAAAATGTCT 8220
Qy CGCTCCTCATCGCTGGGAGTACTGCTTTGATCATATGCGAAGCGGCTGTGCGGATCCTA 8355
Db CGCTCCTCATCGCTGGGAGTACTGCTTTGATCATATGCGAAGCGGCTGTGCGGATCCTA

Db 8221 CGCTTCTCATAGCCGCGATGACTGTTTGATCATATGCGAAGCGGCGAGTGTGCGACCTT 8280
Qy GCGAGCTTTTGGGAGAGCCCTGGGAGAGCTACGGGTACCGATGCGAGCCCTGCTATCATG 8415
Db GCGAGCTTTTGGGAGAGCCCTGGGAGAGCTACGGGTACCGATGCGAGCCCTGCTATCATG 8340
Qy CATCACTGSAACAGCCGCCCTTCTGCTCCACTTGGCTAGCTGAGTGAATGAGAGTGGGA 8475
Db CATCACTGSAACAGCCGCCCTTCTGCTCCACTTGGCTAGCTGAGTGAATGAGAGTGGGA 8400
Qy AACGCAATTTCTTCTGACACCGGACTTTCGAGGCGCCCTCGCTGCGATGTGCGAGGAGT 8535
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Qy CACGCTGGTTCATCTCCTCAGCTGCTCAGCTGCGCGCTTTCAGGGTGGTGGCACACCT 8655
Db CACGCTGGTTCATCTCCTCAGCTGCTCAGCTGCGCGCTTTCAGGGTGGTGGCACACCT 8580
Qy CTGATCTGTGTGTGCGCAGGTACATGTAATTAATCTACAAAGTTTCCACTGGACAACTGC 8715
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Qy CTAACATCATCTGCGCTCCAGGACGAGCGTTGAGGGTTACCGGAGACACAACTA 8775
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RESULT 14
US-08-444-733-182
; Sequence 182, Application US/08444733
; Patent No. 5824507
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsuh P.
; APPLICANT: Wages, John
; APPLICANT: Young, Lavonne M.
; APPLICANT: Fry, Kirk E.
; APPLICANT: Linnen, Jeffrey M.
; TITLE OF INVENTION: Hepatitis G Virus and Molecular
; Cloning Thereof
; NUMBER OF SEQUENCES: 277
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,733
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/389,886
FILING DATE: 15-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/357,509
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,729
FILING DATE: 26-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,271
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/285,558
FILING DATE: 03-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/285,543
FILING DATE: 03-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/246,985
FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0201.36/G100P11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
LENGTH: 9103 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: HGV-JC Variant
FEATURE:
NAME/KEY: CDS
LOCATION: 276..9005
US-08-444-733-182

Query Match 82.6%; Score 7760.6; DB 1; Length 9103;
Best Local Similarity 90.8%; Pred. No. 0;
Matches 8264; Conservative 0; Mismatches 839; Indels 0; Gaps 0;

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Db 421 GGGGTAGCCCAAGAATCTTCGGGTGAGGCGGGGTGGCAATTTCTCTTTCTATACCATCA 480
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QY 556 TGGCAGTCTTCTGCTCTCTCTGTTGAGGCGGGGCGCATTCGGCCCGCGCCACCC 615
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Db 781 TGGGCTGGGTGAGGTACTCTCGGTGTCTAACAGTTGGTGTGCTTACGCGCGCGG 840
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QY 1216 GGCAGTCACTCTCTCGAGGGCTAACGGGTGCGGTATTTCCCACTTGGGGAGAGGGTGTGGG 1275
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QY 1276 ATCGAGGAATGTCACGCTCTTGTGTGACTGCGCCCAACGCGCCCTTGGGTCCCGG 1335
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Db 1201 ACCGTGGGAACGTACGCTCTCTGTGTGACTGCGCCCAACGCGCCCTTGGGTGCGCGG 1260
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Db	3421	CGATATGGGCAACCTCGTTTACGCCCTCGACTTGCAGGCTGAGTCTCTGTGGGTCTATAC	3480
Qy	3356	GATCCAGCAGGGCTTTGTGCCATGCTTGAGCAAGGGGGCAAGGTTGAGCTGGATGTGG	3615
Db	3481	GGTCCAGCAGGGCTTTGTGCCATGCTTGAGTAAGGGAGACAAGTGGAGCTAGATGTGG	3540
Qy	3616	CCATGGAGGTCTCTGACTTCCGTCCGTGGTTCACCGGTCTTGGGACAAAGGCG	3675
Db	3541	CCATGGAGGTCTCAGATTTCCGTGGCTCGTCCGGCTCACCTGTCTTGGCGAGGGGC	3600
Qy	3676	ACGAGTAAGAATGCTGCTGTCAGTGTCCACTCTGGCGGCGAGGGTTACTTGGCGCGCAT	3735
Db	3601	ACGCAGTAGGAATGCTGCTGCTCGGTCTCCACTCGGTGGTTCGCGGTCAACGCGCTCGAT	3660
Qy	3736	TCACTAGGCGGTGACTCAAGTACCAACAGATGCCAAGACTACACAGAACCCCTCCGG	3795
Db	3661	TCACAGGCGGTGGACCAAGTCCCAACAGATGCTAAGAACACCACATGAACCCCCCTCCGG	3720
Qy	3796	TGCGCGCAAAAGAGTTTTCAAGAGGGCCCGTGTGTTATGCTTACCGGGCGGGAAAGA	3855
Db	3721	TGCCGCAAGGAGTTTTCAAGAGAGCCCACTGTTTATGCCACAGGCGCAGGAAGA	3780
Qy	3856	GCACCGCGTACCGTTTGGAGTAGCGGCAACATAGGGCCACAAGGTTCTGATCTTGAACCCGT	3915
Db	3781	GCACGCGCTCCCGTTGGAGTAGTGGCAACATGGGCGACAAGGTCTCTGATTTGAACCCCT	3840
Qy	3916	CGGTAGTACCGTAGGGCCATAGGCCCATACATGGAGCGCTCGCGGGGAAACACCCCA	3975
Db	3841	CGGTGGCGACAGTAGGGCCATAGGCCCTTACATAGAGCGACTCGCGGGAACATCCAA	3900
Qy	3976	GTATTACTGTGCCATGACACACTGCTTTCACAAGGATCACATGACTCGCCCTTACGT	4035
Db	3901	GTATCTACTGTGCCATGACACACTGCTTTCACAAGGATCACATGATTTCCCTTTACGT	3960
Qy	4036	ATTCCACTTACGGAAGTTTTTTGGCCAAACCTTAGGCAGATGCTGAGGGGTGTCTCGGTGG	4095
Db	3961	ACTCTACCTATGGAGGTTTTCTGGCCAAACCTTAGGCAGATGCTCGAGGTGTGTCTCGGTGG	4020
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Qy	4156	GGAGCTGGCGGAGATGTGAGTGCATTTGGTGTCTCTACGCCACATGCGACCCCTCCCG	4215
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Qy	4216	GATCCCCGATGACCCAGCACCCATCAATCATTTGACAAAACTGGAGCTGGGAGATCC	4275
Db	4141	GGTCCCCCATGACTCAGCATCCGTCATCATTTAGACCAAAATTTGATGTGGTGAGATTCT	4200
Qy	4276	CTTTCTATGGGCATGCATACCTCTTTGAGCGGATGCGGACCGGAAGGATCTCGTATTCT	4335
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Db	4441	GGTTAGTGTGGAGAGGTCGTGAGGTGACCCCTTGATCCCAATTAACATCTCCCTGC	4500
Qy	4576	GCACGCTGCCCGCTCGGTGAACCTGCGATGACGCGGAGGACGACGGGTAGGGCA	4635

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Qy	4636	GGTCTGGCGCT	ACTACT	ACGCGGGGGT	CGGAAAGCC	CCCTCT	CGTGGT	TGTTGGCGCT	CAG	4695
Db	4561	GGTCTGGCGCT	ACTACT	ACGCGGGGGT	CGGAAAGCC	CCCGCGG	TGTTGGT	TGCGCTCGG		4620
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Qy	4816	TTGGGGAAG	CGCGGTG	TCTTTTCGGGGCT	TTCGCCGT	TGAGGAT	GCATCCCGAT	GTTA		4875
Db	4741	TCGCTGAAG	CGCGGTG	TTTTTCTCGGGCT	TAGCCCGT	TGAGGAT	GCATCCCGAT	GTTA		4800
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Db	4861	GCGGGAAA	CACATG	CTCCGGACCA	TACGAG	CACCCCAAT	TGGCAG	GTCTGAAGGCC		4920
Qy	4996	CGAATCTGT	CCCACTCCT	GTCTGAGGT	GGGCAATG	ATTACCAT	TAAAGT	TGCGCGGC		5055
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Db	4981	ACCACAT	TTGTGACGAC	CTGGTTCGT	TAGGCTGGCGGAGGGT	TATCTCCGCT	CGG			5040
Qy	5116	ATCGGGA	CCCACTTCTGAT	GGTGGGCGCT	CGCTATT	TGCGGGGGG	GCATGAT	CTATGCGTCA	T	5175
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Qy	5296	GCGCGGGG	GAGAGTCT	CGGCCAT	TCGGATG	CCACACAGT	GACAGAT	CGGT	TGGGGCCA	5355
Db	5221	GCGCGGGG	GAGTCT	CGGCCCTTCG	CCCTTCG	GCATG	CCCAAGACAGT	GCATG	CGGTGGGGCCA	5280
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DB |||||
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DB |||||
QY 7321 TCTCTTATTTGGTCTGGGTGCCATTGACTAGGCGCACCGGCTTAAACACCTGTGG 7380
DB |||||
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DB |||||
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DB |||||
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DB |||||
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DB |||||
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QY 7741 TCTTCAAGACCCAAAGGAAGAGAACGCCCGCTCATTTGTTCCTCCCGCTTGGACT 7800
DB |||||
QY 7876 TCCGGATAGCTGAAAGCTTATTCTGGGAGACCTTGGACGGGTAGCCAGGCGGTGTGG 7935
DB |||||

Db 4081 GGGAGCTGGCAGAGTGTGGGTGCAAGTTGTCTCTACGCCACTGCCACGCCCTCTCG 4140
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Db 4201 CCTCTATGGGCATGGCATACCCCTCGAGCGGATCGGACCGGTAGGACACCTCGTATTCT 4260
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Db 4261 GCTACTCTAAGGCAGAGTGTAGCGGGCTAGCGGGTCAGTTTCTGCTAGGGGAGTTAAG 4320
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Db 4321 CCATAGCCTATTACAGGGGAAGACACTTCTATCATCAAGAGCAGGATGGTGGTGT 4380
QY 4456 GTGCTACAGAGCCACTATCCACTGGGTACACTGGGAACCTCGATTCTGTACCCGATTGTG 4515
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QY 4576 GCACGGTGCCCGCTGCGCTGACTGTCGATGTCAGCGGCGGAGGACGACGGTAGGGCA 4635
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Job time : 200 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2002, 23:11:25 : Search time 10915 Seconds
(without alignments)
18012.351 Million cell updates/sec

Title: US-09-828-498-1
Perfect score: 9395
Sequence: 1 tgacgtgggggggtgatcc.....cccaaagccgggtctact 9395

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
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32: em_htg_other.*
33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description

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4	8100.6	86.2	9395	6	E14141
5	8100.6	86.2	9395	14	D90600
6	8080.6	86.0	9373	14	AF081782
7	8018	85.3	9292	14	AF309966
8	7979	84.9	9392	6	AR026694
9	7979	84.9	9392	6	AR049120
10	7979	84.9	9392	6	AR065378
11	7979	84.9	9392	14	HGU44402
12	7936.8	84.5	9351	14	AF031827
13	7936.8	84.5	9351	14	AF031828
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15	7885.6	83.9	9327	6	AR026878
16	7885.6	83.9	9327	6	AR049304
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18	7760.6	82.6	9103	6	AR026828
19	7760.6	82.6	9103	6	AR049254
20	7760.6	82.6	9103	6	AR065512
21	7760.6	82.6	9103	14	HGU45966
22	7718.2	82.2	9367	14	HGU63715
23	7598.4	80.9	9056	14	AF104403
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT

AX338086
Sequence 1 from Patent WO0177157.
AX338086
AX338086.1 GI:18128718
Hepatitis G virus.
Hepatitis G virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
GBV-C/HGV group.
1 (sites)
Xiang,J., Wuenschmann,S., Schmidt,W. and Stapleton,J.T.
Full-length GB virus C (Hepatitis G virus) RNA transcripts are
infectious in primary cd4 positive T cells and methods of treating
HIV
Patent: WO 0177157-A 1 18-OCT-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
Location/Qualifiers
1. .9395
/organism="Hepatitis G virus"
/db_xref="taxon:45255"
1707 a 2557 c 3004 g 2127 t

ORIGIN

Query Match 100.0%; Score 9395; DB 6; Length 9395;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 9395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	61	CTATCTAAGTAGACGAATGACTCGGGCCGACTCGGCACCGCCCAAGGTGGTGGAT	120						
QY	121	GGGTGGTGACAGGGTTGGTAGGTGCTAAATCCCGGTTCATCTGGTAGCCACTATAGGTGG	180						
DB	121	GGGTGGTGACAGGGTTGGTAGGTGCTAAATCCCGGTTCATCTGGTAGCCACTATAGGTGG	180						
QY	181	GTCTTAAGAGAAGGTCAAGACTCCTTTGTGCTGCGGGAGACCGCGCACGTCCACAG	240						
DB	181	GTCTTAAGAGAAGGTCAAGACTCCTTTGTGCTGCGGGAGACCGCGCACGTCCACAG	240						
QY	241	GTGCTGGCCCTACCGGTGTAATAAGGGCCGACGTGAGCTCGTAAACCCGAGCCC	300						
DB	241	GTGCTGGCCCTACCGGTGTAATAAGGGCCGACGTGAGCTCGTAAACCCGAGCCC	300						
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QY	481	CGCGGGCTCAGCGGGGTAGCCCAAGAAATCTTCGGGTGAGGGGGGTGGCAATTTCTC	540						
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QY	841	ACGTAGCGGGATCCTGGGTCTGGGGAGGTTTACTCCGGGGTCTCAGAGTTGGTGTG	900						
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DB	901	CGTTAGCGCGCGGGTCTACCTGATGCCCAACCTGAAAGTGTGAGTAGAATGTGACGTTA	960						
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DB	1081	TGGTTTGGGTGGCCCGCATTTGCTTGGAGCAACGGATTTGTCATGGTTTTCCTGCTCG	1140						
QY	1141	TCAGGATGCGGGGATGTTGCAAGCGCCCGCTCCGTTTGGGGTCCCGCCCTTTG	1200						
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QY	1201	ACTACGGGTGAAGTGGCAGTCACTCTCTGAGGGCTAACGGGTGCGGTATTTCCCACTG	1260						
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QY	1261	GGGAGAGGTGTGGGATCGAGGGAATGTACGCTCTTGTGTGACTGCCCAAGGCCCT	1320						
DB	1261	GGGAGAGGTGTGGGATCGAGGGAATGTACGCTCTTGTGTGACTGCCCAAGGCCCT	1320						
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DB	1321	GGTTTGGGTCCCGGCTTTTCCAGGCGGTGGGTGGGGCGACCCCATCACCATTTGA	1380						
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DB	1621	TTCTGACGCTCGGCCCTGCTTCATGTGGACCTGTGTGGGGAGTCTGCCCCGAAACCG	1680						
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DB	1681	GGTGGTTAGATTCCCTTCCATCGGTGCGGACCGGGCTCGGCTGACAAAGACTTG	1740						
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DB	1861	TCCGGGATTCCTTGCATTTGGTCAAAATGTCCACACAGCAGCTAGAGCTTCCGACTGAA	1920						
QY	1921	CGTTGGGTCTTCCCGGGAGTCCCGCCCATTAACAACTGCATGCCGCTAGGCAAG	1980						
DB	1921	CGTTGGGTCTTCCCGGGAGTCCCGCCCATTAACAACTGCATGCCGCTAGGCAAG	1980						
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DB	1981	TGCTGAGGCAATTTGGGGAGCTGGGCTTACGGGGGGTCTACGAGCTCTGTTGCA	2040						
QY	2041	GGTGTTCGGAGCTGATGGGACCGGAAATCCCGTTTCCCGGGGTACGATGCTGCT	2100						
DB	2041	GGTGTTCGGAGCTGATGGGACCGGAAATCCCGTTTCCCGGGGTACGATGCTGCT	2100						

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DB 2221 TGAAGCTGGCTGAGGACACGGTTGGTCCCTGTGATCTCTGCTGTGGTGGGTGA 2280
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DB 2281 ACCAGTTGGCGGTTCTAGAGCTGCCGGCTGTGGACGCTGCCGTGGGGGTGAAGTTTTC 2340
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DB 2941 GCGAGAGGCGCACCACTCCGACTGGTCCCAAGATGTGCGCAAGAGGGGCTACCTCT 3000
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DB 3001 TTGACACATGGGCTCTTCTCGCGGCTGTCAAGAGCGCTTGTGGAATGGAGCGCG 3060
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RESULT 2				
LOCUS	AF121950	9395 bp	RNA	linear
DEFINITION	Hepatitis G virus strain Iowan, complete genome.			
ACCESSION	AF121950			
VERSION	AF121950.1	GI:4884678		
KEYWORDS	Hepatitis G virus.			
SOURCE	Hepatitis G virus			
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; GBV-c/HGV group.			
REFERENCE	1 (bases 1 to 9395)			
AUTHORS	Xiang,J., Wunschmann,S., Schmidt,W., Shao,J. and Stapleton,J.T.			
TITLE	Full-length GB virus C (Hepatitis G virus) RNA transcripts are infectious in primary CD4-positive T cells			
JOURNAL	J. Virol. 74 (19), 9125-9133 (2000)			
MEDLINE	20438110			
PUBMED	10982359			
REFERENCE	2 (bases 1 to 9395)			
AUTHORS	Xiang,J.H., Schmidt,W.N., Labrecque,D.R. and Stapleton,J.T.			
TITLE	Direct Submission			
JOURNAL	Submitted (21-JAN-1999) Internal Medicine, Iowa City Veterans			

Administration Medical Center, The University of Iowa, SW54, GH, Iowa City, IA 52242, USA		Location/Qualifiers	
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		CTGAAGACTCAGAACCTGACTGAGGCCGACCTCCGCCGGGGCTGCGAGCCCTTCAGGCTA	
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		TCGAGAATGCTCGGAGAAATCTTTGAACCTCACAATAGATGTCATCATGGAAGATTGCAGTA	
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		CTCCATCGCCAGCACTTATCTCGTTACTGAGAGAGCCCAAGATGAGAAGACCCCTCGG	
Qy	7021	TGTCCTTCGAGGAGGATACCCGCTCTCTGACTCATCTTCGAGGTGCATCCAGAGTCCG	7080
Db	7021		7080
		TGTCCTTCGAGGAGGATACCCGCTCTCTGACTCATCTTCGAGGTGCATCCAGAGTCCG	
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Db	7081		7140
		AGACGCCGAAGGGAGGAAACGCTCTCAACGTGGCTCTTTCGGTACTAAAAAGCCTTGT	
Qy	7141	TTCCACAGAGCGATGCCACAAGAAAGCTTACCGTTAAGATGTCAATGCTGTTGAGAAGA	7200
Db	7141		7200
		TTCCACAGAGCGATGCCACAAGAAAGCTTACCGTTAAGATGTCAATGCTGTTGAGAAGA	
Qy	7201	GCCTAACACGCTCTCTTTCATTGGGATTTGACGGTCGCTGACGTGGCAAGCCTGTGTGAGA	7260
Db	7201		7260
		GCCTAACACGCTCTCTTTCATTGGGATTTGACGGTCGCTGACGTGGCAAGCCTGTGTGAGA	
Qy	7261	TGAAATCCAGAACCATACAGCCTATTGTGACAAAGTGCCGACCTCCGCTTGAATTCGAGG	7320
Db	7261		7320
		TGAAATCCAGAACCATACAGCCTATTGTGACAAAGTGCCGACCTCCGCTTGAATTCGAGG	
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Db	7321		7380
		TTGGGTGCTTGGTGGCAATGAACCTTTGTAATGTGACAAAGTGAAGCTTAGGCTAGGCAAG	
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Dz	.8521	CGATGTCGAGCGAGTACAGTGACCAATGGCTTGGGCCATCGGTTACATCTCTCTATACC	8580
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RESULT 3
D87255
LOCUS D87255 Hepatitis G virus RNA for polyprotein, complete cds. VRL 07-FEB-1999
DEFINITION Hepatitis G virus (isolate: HGV-Iw) cDNA to genomic RNA.
ACCESSION D87255
VERSION D87255.1 GI:1731799
KEYWORDS polyprotein.
SOURCE Hepatitis G virus (isolate: HGV-Iw) cDNA to genomic RNA.
ORGANISM Hepatitis G virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
GBV-C/HGV group.
1 (bases 1 to 9375)
Shao, L.
Direct Submission
Submitted (20-AUG-1996) Li Shao, Yamagata University School of
Medicine, 2nd Department of Internal Medicine; Iida-nishi 2-2-2,
Yamagata, Yamagata 990-23, Japan
(E-mail: shori@med.id.yamagata-u.ac.jp, Tel: 0236-28-5309,
Fax: 0236-28-5311)
2 (bases 1 to 9375)
Shao, L., Shinzawa, H., Zhang, X. and Takahashi, T.
Complete nucleotide sequence of hepatitis G virus isolated from a
Japanese patient with non-A, non-B, non-C, and non-E hepatitis
unpublished (1997)
3 (sites)
Shao, L., Shinzawa, H., Ishikawa, K., Zhang, X., Ishibashi, M.,
Misawa, H., Yamada, N., Togashi, H. and Takahashi, T.
Sequence of hepatitis G virus genome isolated from a Japanese
patient with non-A-E-hepatitis: amplification and cloning by long

reverse transcription-PCR
Biochem. Res. Commun. 228 (3), 785-791 (1996)
97096330
Sequence
updated (05-Nov-1996) by Li Shao.
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BASE COUNT 1674 a 2556 c 2994 g 2151 t
ORIGIN

Query Match 86.3%; Score 8106.4; DB 14; Length 9375;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 8589; Conservative 0; Mismatches 786; Indels 1; Gaps 1;
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DB 6900 TAGCCGAGAGTGCCTGTGTGGGAGAGACATACCCCGCACTCATCGCCAGCACTTAT 6959
QY 6980 CTCGGTTACTGAGACAGCCCAATGAGAAGACCCCGTGGTGTCTTCTCGCAGGAGA 7039
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LOCUS E14141 9395 bp RNA linear PAT 28-JUL-1999
DEFINITION Genomic sequence of GBV-C/HGV.
ACCESSION E14141
VERSION E14141.1 GI:5708824
KEYWORDS JP 1997276000-A/2.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 9395)
AUTHORS Okamoto,H.
TITLES HEPATITIS NON-A NON-B NON-C VIRAL GENE NUCLEOTIDE AND DETECTION
JOURNAL Patent: JP 1997276000-A 2 28-OCT-1997;
NATSUKU:KK
COMMENT OS GBV-C/HGV
PN JP 1997276000-A/2
PD 28-OCT-1997
PF 18-APR-1996 JP 1996134117
PI OKAMOTO HIROAKI
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CC anti-sense: No;
FH Key
FH Location/Qualifiers
FT source 1..9395
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FEATURES
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QY	3301	GTAGGATCCTGACTTTACATCCAGGAAACGTATGGTTTGGGACGGCTACCTACAGAA	3360
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Db	3421		
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Immunology Division; Minamikawachi-machi, Kawachi-gun, Tochihi
329-04, Japan (E-mail:hokamoto@jichi.ac.jp,
Tel:0285-44-2111(ex.3334), Fax:0285-44-1557)
2 (sites)
Okamoto,H.
Unpublished (1996)
3 (sites)
Okamoto,H., Nakao,H., Inoue,T., Fukuda,M., Kishimoto,J., Iizuka,H.,
Tsuda,F., Miyakawa,Y. and Mayumi,M.
The entire nucleotide sequences of two GB virus C/hepatitis G virus
isolates of distinct genotypes from Japan
J. Gen. Virol. 78 (Pt 4), 737-745 (1997)
97275884

FEATURES

Location/Qualifiers

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Db 5881 TGTGATGCGCATCCCGTGTCTAACAGTCTGGGGCGGGCTTGGCGGGATCGCTCTTG 5940
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RESULT 6

AF081782

LOCUS

DEFINITION

AF081782

VERSION

KEYWORDS

AF081782 9373 bp RNA linear VRL 05-JAN-1999
Hepatitis G virus strain HGV-Iw isolate phgVdz, complete genome.
AF081782
AF081782.1 GI:4093140

SOURCE	Hepatitis G virus.
ORGANISM	Hepatitis G virus
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; GBV-C/HGV group.
AUTHORS	1 (bases 1 to 9373)
TITLE	Zhu,F.L., Qi,Z.T., Shao,L., Ren,H. and Song,Y.B. Splicing and cloning of the full-length genomic cDNA of GB virus C/hepatitis G virus
JOURNAL	Ti Erh Chun i Ta Hsueh Hsueh Pao 19, 301-306 (1998)
AUTHORS	2 (bases 1 to 9373)
TITLE	Zhu,F.L., Qi,Z.T., Shao,L., Ren,H. and Song,Y.B. Direct Submission
JOURNAL	Submitted (31-JUL-1998) Department of Microbiology, Second Military Medical University, 800 Xiang Ying Road, Shang Hai 200433, China
REFERENCE	3 (bases 1 to 9373)
AUTHORS	Zhu,F.L., Qi,Z.T., Shao,L., Ren,H. and Song,Y.B. Direct Submission
TITLE	Submitted (04-JAN-1999) Department of Microbiology, Second Military Medical University, 800 Xiang Ying Road, Shang Hai 200433, China
REMARK	Sequence update by submitter
COMMENT	On Jan 5, 1999 this sequence version replaced gi:3421387.
FEATURES	Location/Qualifiers
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Db	8219	ACCTGCTACATTAAGGTGAAGCCGCTGTGAGAGGTGGGGCTGAAAATGTCTCACTC	8278	Db	9299	CGGATGGGCAAGTGCACCTGTGATCTGAGGGGTGCACCCCGGTAAGAGCCCGGCCCAA	9358
QY	8301	CTCATCTGCGGATGACTGTTTGCATCATATGCGAAGCGCTGTGCGGATCCTTAGCGAC	8360	QY	9381	AGCCCGGTTCTTACT 9395	
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QY	8361	GCTTTGGCAGAGCCCTGGCGGCTACGGGTACGATCGAGCCTTCGTATCATGTCATCA	8420	RESULT 7			
Db	8339	GCTCTGGCAAGCGCTATCAAGTATGGGTACGCTGCGAGCCTTCATATCATGTCATCA	8398	AF309966	Hepatitis G virus isolate PEI	9292 bp	RNA linear VRL 25-OCT-2000
QY	8421	CTGACACGGCCCTTCTGCTCCACTTGGCTAGCTGAGTGAATGAGATGGGAACGC	8480	LOCUS	AF309966	cds.	
Db	8399	TGGACACGGCCCTTCTGCTCCACTTGGCTCGCTGAGTGAATGAGATGGGAACGC	8458	DEFINITION	AF309966	Hepatitis G virus isolate PEI.	
QY	8481	CATTTCCTCTGACACGAGCTTTCGAGGCCCCCTCGCTGCGATGTCAGCGAGTACAGT	8540	ACCESSION	AF309966.1	GI:10998817	
Db	8459	CATTTCCTCTGACACGAGCTTTCGAGGCCCCCTCGCTGCGATGTCAGCGAGTACAGT	8518	VERSION	AF309966.1	KEYWORDS	
				SOURCE		Hepatitis G virus isolate PEI.	
				ORGANISM		Hepatitis G virus isolate PEI	
						Viruses: ssRNA positive-strand viruses, no DNA stage; Flaviviridae; GBV-C/HGV group.	

REFERENCE 1 (bases 1 to 9292)
AUTHORS Kempfer,M., Nuebling,M.C. and Loewer,J.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2000) FG 2/4, Paul-Ehrlich-Institut,
Paul-Ehrlich-Str. 51-59, Langen 63225, Germany

FEATURES
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QY	182	TCCTTAAGAGAGAGGTCAAGACTCCTCTGTGCTCGCGCGAGACCGCGCACGGTCCACAGG	241
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Db	3302	TCGGGAYCCCTGACTTACATCCAGGAAACGTATGCTTTGGRACGGCTACGTCCGGAAG	3361
Qy	3362	CATGGGGACATGTCGTGAATGGGCTGCTGTTTACAACCTTTTCATATGGGGTTCATCCCGAAC	3421
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Qy	4262	CGTGGGAGATCCCCTTCTATGGGCATGGCATACCTCTTGAGCGGATGCGGACCGGAAG	4321
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DB	5102		5161
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DB	5282		5341
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QY	5402	AGTCTGTCTTGGCCACGCGCTAAGACGGCCGAGGCGCTACCGAGCTTACCACCAAGTGGCT	5461
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Db 8162 GACYCCGAAGGGGTGCCAGTGGGTGAGAGTATTGTAGGTCTCTCGGAGCTTTGACTAC 8221
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Db 8822 TGGCCTAGCAGTCCACCGGAAGAGCGTGRGCTGTGCGACGCGCATCTCCGGTCCGR 8881
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RESULT 8
AR026694 LOCUS AR026694 9392 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5856134.
ACCESSION AR026694
VERSION AR026694.1 GI:5937534
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9392)
AUTHORS Kim, J. P., Fry, K. E., Young, L. Marie., Linnen, J. M. and Wages, J.
TITLE Hepatitis G virus and molecular cloning thereof
JOURNAL Patent: US 5856134-A 14 05-JAN-1999;
FEATURES
source location/Qualifiers
1. 9392
BASE COUNT 1694 a 2551 c 2998 g 2148 t 1 others
ORIGIN

Query Match 84.9%; Score 7979; DB 6; Length 9392;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 8515; Conservative 1; Mismatches 876; Indels 1; Gaps 1;
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Qy 123 GTGGTGACAGGGTGGTAGGTGCTAAATCCCGGTCAATCTGGTAGCCACTATAGGTGGGT 182
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QY 363 ACCAATAGGTTTATCCCGCCGAGTTGACAAGACAGTGGGGCCGGGGTGTATGGGAAG 422
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QY 423 GACCCCAACCTGCCCTTCCCGTGGGCCGGGAATGCAATGGGGCCACCGAGTCCGCG 482
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Qy	6963	CCATCGCGAGCACTTATCTCGGTACTGAGAGCAGCCAGATGAGAAGACCCGCTCGGTG	7022
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Qy	7023	TCCTTCCTCGCAGGAGATACCCCGCTCTCTGACTCATTCGAGGTCAATCCAAAGAGTCCGAG	7082
Db	7020	TCCTTCCTCGCAGGAGATACCCCGCTCTCTGACTCATTCGAGGTCAATCCAAAGAGTCCGAG	7079
Qy	7083	ACAGCCGAAGGGAGGAAGCGTCTTCAACGTGGCTCTTCCGTACTAAAGACCTTGTTT	7142
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Qy	7143	CCACAGAGCATGCCACAAGAAAGCTTACCCTTAGATGTATGCTGTGTGAGAAAGC	7202
Db	7140	CCACAGAGCATGCCACGAGGAAGCTTACCCTCAAGATGTCTGCTCGCTTGAAGAGC	7199
Qy	7203	GTAAACAGCTCTCTTTTCATTTGGGATGTACGGTCGCTGACGTGGGAAGCCTGTGTGAGATG	7262
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Db	7260	GAATCCAGNACCATACACCTTATGTGACCAGTGGCACTCGCTTGTAATTCAGGTT	7319
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Db	7320	GGGTGCTTGGTGGCAATGAACCTTACCCTTGAATGTACAAGTGTAGGCTTAGGCAAGAA	7379
Qy	7383	ACCTTGGCTTCTTCTTACATTTTGGTCTGGGTGCCACTGACAGGGGCCACTCCGGCC	7442
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Qy	7443	AAGCCCTCTGTGTGAGCGCGTGGCTCTTCTGTGTGGCGGACACCAACCAAGTGTAT	7502
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Db	7560	AGGTTTCATGATTAAGTACCTCTGTGACTCTATTGAGCGGCTTAGAGGGCGCTCAAGCC	7619
Qy	7623	TGCTTAAGCATGGGTTTACACTTATGAGGAGGCAATTAAGGACTGTAAAGGCCACATGCTGCC	7682
Db	7620	TGCCTAAGCATGGGTTTACACTTATGAGGAAGCAATAAGSACTGTAAGSACCACATGCTGCC	7679
Qy	7683	ATGGGCTGGGATCTAAGGTGTCTGATCAAGGACTTCGCCACCCCTCGGGGGAAGATGGCT	7742
Db	7680	ATGGGCTGGGATCTAAGGTGTCTGATCAAGGACTTCGCCACCCCGGGGGAAGATGGCC	7739
Qy	7743	GTCCATGACCGGCTCCAGGAGATCTTGAAGGAGCGCAGTCCCTTTTACTCTTACTGTG	7802
Db	7740	GTCCATGACCGGCTCCAGGAGATCTTGAAGGAGCTCCGGTCCCTTTTACTCTTACTGTG	7799
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RESULT 9
AR049120
LOCUS AR049120 9392 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 14 from patent US 5824507.
ACCESSION AR049120
VERSION AR049120.1 GI:6005159
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9392)
AUTHORS Kim,J.P., Fry,K.E., Young,L.Marie, Linnen,J.M. and Wages,J.
TITLE Hepatitis G virus and molecular cloning thereof
JOURNAL Patent: US 5824507-A 14 20-OCT-1998;
FEATURES
Location/Qualifiers
source
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/organism="unknown"
BASE COUNT 1694 a 2551 c 2998 g 2148 t 1 others
ORIGIN

Query Match 84.9%; Score 7979; DB 6; Length 9392;
Best Local Similarity 90.7%; Pred. No. 0;
Matches 8515; Conservative 1; Mismatches 876; Indels 1; Gaps 1;

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QY 63 ATCTAAGTAGACCAATGACTCGGCGCGACTCGGCGACCGCGCAAAAGGTGGTGATGG 122
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QY 123 GTGGTGACAGGGTGGTAGTTCGTAATCCCGGTATCTCTGTGTAGCCACTATAGTGGGT 182
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Db 121 GTGATGACAGGGTGGTAGTTCGTAATCCCGGTACCTTGGTAGCCACTATAGTGGGT 180
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QY 243 GCTGGCCCTACCGGTGCTGAATAAGGGCCGACGTGAGGCTCGTCTAAACCGAGCCCGT 302
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Db 361 ACCAATAGGCGTAGCGCGGAGTTGACAAGGACCAGTGGGGCCGGGGCT-TGGAGAGG 419
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QY 423 GACCCCAAAACCTGCCCTTCCCGGTGGCGGGAATGATGGGGCCACCCAGCTCCGG 482
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Qy	1383	CAGG	CAAAACCAAGTGGCCCTATCATGCCCCCAATATGCTATGGGCTGTGTCTCCGTA	1442
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Qy	1503	GATG	TGTGGAGTTGGTGGCGGTGGATGTCGCAAGCTGCACATAGCGGCTGTAGGCTCA	1562
Db	1500	GATG	TGTGGAGTTTAGTGGCCAGTTGGCTCTGCGCACTGCACATAGCGCACTTGGATCA	1559
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Qy	1623	CTG	ACCGTGGGCTCTTCATGTGGCACTGTGTGGGAGCTGTGCGCCGCAAAACCGGG	1682
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Qy	1683	TCG	GTAGATTCCCTTCCATCGGTGCGGACGGGGCTCGGCTGTACAAAGAGACTTGGAA	1742
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Qy	1743	GC	TGCCCCCTGCTCAACAGGACAACCTCCCTTCACCATTAAGGGGCCCTTGGCAACCG	1802
Db	1740	GC	TGCCCCCTGCTCAACAGGACAACCTCCCTTCACCATTAAGGGGCCCTTGGCAACCG	1799
Qy	1803	GG	GAGGCAACCGGTGGGGCTCGGCCCTTGGGTTTTGGGTCTTACACCATGACCAAGATC	1862
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Qy	1923	TT	CGGGTTCTTCCCGGAGTCCCGCCATTAAACAATGCATCGCGCTAGGCAGCGAAGTG	1982
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Qy	2283	C	AGTTGGCGGTTCTAGACTGCGGGCTGTGAGAGCTGCGCTGGCGGGTGAAGTTTTCGG	2342
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Qy	2343	G	GCCTGCCCTGTGATGGTGTGGGCCCTCCCACTGTCAGTATGATAGTAGGCTAGCA	2402
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ACCESSION AR065378
VERSION AR065378.1 GI:5995594
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9392)
AUTHORS Kim,J.P.; Fry,K.E.; Young,L.Marie.; Linnen,J.M. and Wages,J.
TITLE Hepatitis G virus and molecular cloning thereof
JOURNAL Patent: US 5849532-A 14 15-DEC-1998;
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DEFINITION	Hepatitis G virus, complete genome.		
ACCESSION	U44402		
VERSION	U44402.1	GI:1167560	
KEYWORDS	Hepatitis G virus.		
SOURCE	Hepatitis G virus.		
ORGANISM	Hepatitis G virus.		
REFERENCE	Viruses: ssRNA positive-strand viruses, no DNA stage: Flaviviridae;		
AUTHORS	1 (bases 1 to 9392)		
	Linnen, J., Wages, J., Zhang-Keck, Z.-Y., Fry, K. E., Krawczynski, K.,		
	Alter, H., Koonin, E., Gallagher, M., Alter, M., Hadziyannis, S.,		
	Karayiannis, P., Fung, K., Nakatsuji, Y., Shih, W.-K., Young, L.,		
	Piatak, M. Jr., Hoover, C., Fernandez, J., Chen, S., Zou, J.-C.,		
	Morris, T., Hyams, K. C., Ismay, S., Lifson, J. D., Hess, G.,		
	Fong, S. K. H., Thomas, H., Bradley, D., Margolis, H. and Kim, J. P.		
TITLE	Molecular cloning and disease association of hepatitis G virus: a		
	transfusion-transmissible agent		
JOURNAL	Science 271 (5248), 505-508 (1996)		
MEDLINE	96152370		
REFERENCE	2 (bases 1 to 9392)		
AUTHORS	Linnen, J.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-JAN-1996) Jeff Linnen, Genelabs Technologies, Inc.,		
	505 Penobscot Dr., Redwood City, CA 94063, USA		
COMMENT	Corresponding author for this submission is Jungsoh P. Kim.		
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	RIVVFLTWAGMSGAPASVLGSPDFDGLTWQTCSCRANGRSFTEGKWDNRGNV		
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QY 2463 AAGCTCGCTGGGAGCTTTCCGCTGCGACTTTTGTATGGGATTTCCGCGACCCGCGG 2522
DB 2460 AAGCTCGCTGGGAGCTTTCCGCTGCGCTTCTTGTATGGGATTTCCGCGACCCGCGG 2519
QY 2523 CCGACCTTCTGCTCGGGCGGAGTTCTGCTGATGTCACATTCGAGTGGACACTTCG 2582

Db 2520 CCGACCTCAGTGCTCGGGCCCGAGTTCTGCTTCGATGCTACATTCGAGGTGGACACTTCG 2579
Qy 2583 GTGTTGGCTGGGTGGCCAGCTGGTGGCTTGGCCATAGCCCTCTGAGCTCAATG 2642
Db 2580 GTGTTGGCTGGGTGGCCAGTCTGGTAGCTTGGCCATTCGCCCTCTGAGCTCGATG 2639
Qy 2643 AGCGAGGGGGTGAAGCAAGGCCGCTGATCTATAGACGTGTGTAAAGGCTACCAAG 2702
Db 2640 AGCGAGGGGGTGAAGCACAAAGCCGCTGATCTATAGACGTGTGTAAAGGGGTACCAAG 2699
Qy 2703 GCTGTGCCAGAGAGGTGTGGGAGCCCTCTCGGGAGGGGCGTCTACCAAGCTTCG 2762
Db 2700 GCAATCCGTCAAGGGTGTGAGGAGCCCTCTCGGGAGGGGCGCCCTGCAAAACCCCTG 2759
Qy 2763 AGTTTCGCTGTGCTTGGCCCTCATACATCTGGCCGGATGCTGTGATGATGCTGTGGTG 2822
Db 2760 ACCTTTGCTGTGCTTGGCCCTCTACATCTGSCCAGATGCTGTATGATGCTGTGGT 2819
Qy 2823 GCCTTGTCTCTCTTGGCCCTGTTCGACGCACTTGGACTTGGCCCTGGAGAGTCTCTG 2882
Db 2820 GCCTTGTCTCTCTTGGCCCTGTTCACGCGTGTGGATTTGGCCCTTGGAGGAGATCTTG 2879
Qy 2883 GTCCTCCGSCCTCTTACGGCACTGGCAGCGGTGTGAGTGTGCTGTGATGGCGGC 2942
Db 2880 GTGTCCTGGCCCTCTGTTCGGCGTTTGGCTCGGGTGGTGTGATGCTGTGATGGCGGT 2939
Qy 2943 GAGAAGGCCACCACTCCGACTGTCTCCAAGATGTGCGCAAGAGGGCCCTACCTGTTT 3002
Db 2940 GAGAAGGCCACACCGTTCGGCTGTCTCCAAGATGTGCGCAGAGGAGCTTATTTGTTT 2999
Qy 3003 GACCACATGGGCTCTTTCGCGCTGTCAAGAGCGCTTGTGGAATGGGACGCGCT 3062
Db 3000 GATCATATGGGCTCTTTTTCGGCTGTCTGTCAGGAGCGCTTGTGGAATGGGACGAGCT 3059
Qy 3063 TTGGAGCCCTTGTCTATTACTAGGAGCACTGTCCCATCATCAGAGATGCCCGAGGACC 3122
Db 3060 CTGAACCTGTCTATTCACTAGGAGCACTGTCCCATCATACGGGATGCCCGAGGACT 3119
Qy 3123 CTGTCTCGGACGTGGCTATGGTTTACCGTGTGAGCAGCGCGGTGATCAGGTT 3182
Db 3120 TTGTCCTCGGCACTGGCTCATGGTTTACCGTGTGCGCGCTGGTGTGATGAGGTT 3179
Qy 3183 CTCATCGGCGTCTTCAGGATGTGAATCATTTGCCCTCCCGGTTGTCCCGACTCACCA 3242
Db 3180 CTCATCGGCGTCTTCAGGATGTGAATCATTTGCCCTCCCGGTTTTCGACCGCGCT 3239
Qy 3243 GTTGTATCCGCTGGTGGGAAGGCTTCTGGGGGTACAGAGCAGCCTTGACAGT 3302
Db 3240 GTTGTATCCGACGTGGGAAGGCTTCTTTGGGGGTACAAAGGCTGCCCTTGACAGT 3299
Qy 3303 AGGGATCCTGACTTACATCCAGGGAACGTCTATGTTGGGACGCTACGTCACGAAGC 3362
Db 3300 CGGGATCTGACTTACATCCAGGGAACGTCTATGTTGGGACGCTACGTCGCGAAGC 3359
Qy 3363 ATGGCACATGTCTGAATGGCTGTGTTCACAACTTTCCATGGGGCTTCATCCGAAAC 3422
Db 3360 ATGGGAACATGTCTGAACGGCTGTCTTTCAGACCTTCCATGGGGCTTCATCCCGAAC 3419
Qy 3423 ATCGCCAGCCGCTGGGGCCCTTAAATCCAGGTGGTGTACGACAGTATGACGCTCAG 3482
Db 3420 ATCGCCACACCGTGGGGCCCTTAAATCCAGATGGTGTACGACGAGTATGATGTCAG 3479
Qy 3483 GTGTACCGCTTCCAGATGGGCACTTCGTTGAGCCCTGCACCTTGCAGCGGAGTCC 3542
Db 3480 GTGTATCCACTCCCGATGGGGCTACTTCGTTAACACCTTGTACTTGCAGGCTGAGTCC 3539
Qy 3543 TGTGGGTATTAGATCCGACGGGCTTTGTGCCATGGCTTGAGCAAGGGGACAAAGGTT 3602
Db 3540 TGTGGGTATCATGATCCGACGGGCCCTATGCCATGCTTGAACAAGGGGACAAAGTG 3599
Qy 3603 GAGCTGGATGTGGCCATGAGAGTCTCTGACTTCCTGGTGTCTGTGTTTACCGGTCCTT 3662
Db 3600 GAGCTGGATGTGGCCATGAGAGTCTCTGACTTCCGCTGGCTCTGTGGCTCACCGGTCCTA 3659

Qy 3663 TCGCAAAAGGCGACGACAGTAAGAATGCTGCTCAGTCTCCACTCTGGCGCAGGGTT 3722
Db 3660 TGTGACGAAGGCGACGACAGTAGAATGCTGCTGTGCTTCACTCCGCTGGTAGGGTC 3719
Qy 3723 ACTGGGCGCGATTCACATAGGCCGTGGACTCAAGTACCACAGATGCCAAGACTACCA 3782
Db 3720 ACCGGGCGCGGTTCACTAGGCCGTGGACCAAGTACCACAGATGCCAAGACTACT 3779
Qy 3783 GAACCCCTCGCGTCCGGCAAAAGAGTTTCAAGGAGGCCCGCTGTTTATGCTAG 3842
Db 3780 GAACCCCTCGCGTCCGGCCAAAGAGTTTCAAGAGGCCCGCTGTTTATGCTAG 3839
Qy 3843 GGGGCGGAAGAGACCCCGCTACCGTTTGGAGTACGGCAACATGGGCCACAAAGTCTTG 3902
Db 3840 GGAGCGGAAGAGACACACGCTCGCGTCCGTTGGAGTAGATAAATGGGCGACAAGTCTTA 3899
Qy 3903 ATCTTGAACCCCTCGGTAGCTACCGTGGGGCCATGGGCCCATATGAGGCGGTGGG 3962
Db 3900 ATCTTGAACCCCTCAGTGGCCACTGTGGGGCCATGGGCCCATATGAGGCGGTGGG 3959
Qy 3963 GGAAGAACCCCGATTTACTGTGCCCATGACACACTGCTTTCACAAGAGTCACTGAC 4022
Db 3960 GGTAAACATCCAAGTATATACTGTGGGCATGATACAACCTGCTTTCACAAGGATCACTGAC 4019
Qy 4023 TCGCCCTTACGATTTCCACTTACGGAAGGTTTTTGGCCAAACCTAGGCAGATGCTGAG 4082
Db 4020 TCCCCCTCAGCTATTCACCTATGGAGGTTTTTGGCCAAACCTAGGCAGATGCTACG 4079
Qy 4083 GTGTGTGGTGGTCAATTTGTGACGAGTCCACAGTCAATGACTCAACTGTGTTGTTGGC 4142
Db 4080 GCGCTTTCGGTGTCAATTTGTGATGATGCCACAGTCACTCAACCGTCTGCTTAGCG 4139
Qy 4143 ATTGGGCGTGTACGAGGCTGCGCGAGGATGTGGAGTCAATTTGGTGTCTACGCCACT 4202
Db 4140 ATTGGGAGATCCGGAGCTGCGCGTGGTGGGGTGCAACTAGTGTCTACGCCACC 4199
Qy 4203 GGCACCCCTCCCGATCCCGATGACCAAGACCCATCAATCATTTAGACAAACTGGAC 4262
Db 4200 GCTACACCTCCCGATCCCTATGACGACACCCCTTCCATANTTGAACAANATGGAC 4259
Qy 4263 GTGGAGAGATCCCTTCTATGGGATGGCATACCTTCTTGAGCGGATCGGACCGGAAG 4322
Db 4260 GTGGGAGATTCCTCTTTTATGGGATGGAATACCCCTCGAGCGGATGCGAACCGAAG 4319
Qy 4323 CATCTGCTATTCGCCACTCCAAAGCTGAGTGGAGCGCTGCGGGCGGAGTTTCGGCT 4382
Db 4320 CACCTCGTGTCTGCAATTTAAGGCTGAGTGGAGCGCTTGTCTGGCCAGTTCTCCGCT 4379
Qy 4383 AGGGGGTAAATGCCATCGCTTATACAGGGGAAGACAGTTCTATCATCAAGATGA 4442
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Qy 4503 GTCACCGATTGTGGTTAGTGTGGAGAGGTCGTGAGGTGACCCCTTGATCCCACTTT 4562
Db 4500 GTCACCGATTGTGGATTAGTGTGGAGAGGTCGTGAGGTGACCCCTTGATCCCACTTT 4559
Qy 4563 ACCATCTCCCTCCGACGCGTCCCGCTGCGCTGAGTGTGATGTCAGCGGGGAGGACGC 4622
Db 4560 ACCATCTCCCTCCGACAGCTGCTGCTGCGGTGAACCTGCTGATGCAAGAGAGGACGC 4619
Qy 4623 AGGGTAGGGAGGCTCTGGCGCTACTACTACGCGGGGTTCGCAAGGCCCTCTGCTGT 4682
Db 4620 AGGGTAGGGAGGCTCTGGAGCTTACTACTACGCGGGGTGGGCAAGCCCTTCGGGT 4679
Qy 4683 GTGTGCGCTCAGGTCCTGTCTGTGTCGGCGGTGGAAGCGGTGTGACCTGTGACGGAATG 4742
Db 4680 GTGTGCGCTCAGGTCCTGTCTGTGTCGGCGGTGGAAGCTGGAGTGGTACCTGGTACGGAATG 4739

Qy	4743	GAACCTGACCTGACACAAACCTACTGAGACTTTACGACAACTGCCCTTACACCGCAGCC	4801
Db	4740	GAACCTGACTTGACAGCTAACTACTGAGACTTTACGACGACTGCCCTTACACCGCAGCC	4799
Qy	4803	GTGCGAGCTGACATTTGGGGAAGCCGGGTGTTCTTTTCGGGGCTTGCCCGTTGAGGATG	4862
Db	4800	GTGCGGGCTGATATCGGAAGAAGCCGGGTGTTCTTCTGCGGCTCGCCCATTTGAGGATG	4859
Qy	4863	CATCCCGATTTAGCTGGCGAAAAGTTGCGGGCTCAACTGGCCCTTCTCGTGGGTGTTT	4922
Db	4860	CACCTGATGCTAGCTGGCAAAAGTTGCGGGCTCAACTGGCCCTTCTGTTGGGTGTTT	4919
Qy	4923	CAGCGACCATGTGCCGGAAACACTGTCTCCGGCCCATCGATGACCCCCACAGTGGGCA	4982
Db	4920	CAGCGACCATGTGTCGGAAACACTGTCTCCGGCCCATCGATGACCCCCAATGGGCA	4979
Qy	4983	GGTCTGAAGGCCCGAATCCTGTCCCACTCTGCTGAGGTGGGCAATGATTTACCATCT	5042
Db	4980	GGTCTGAAGGCCCAATCCTGTCCCACTCTGCTGAGGTGGGCAATGATTTACCATCT	5039
Qy	5043	AAAGTGGCGGCCCATCACATCTGTGACGACCTTGGTCCCTGAGCTCGGGGTGGCGAGGGT	5102
Db	5040	AAAGTGGCGGCCACACATAGTGGACGACCTGGTCCCGGAGACTCGGTGGCGAGGGT	5099
Qy	5103	TAGTTCGCTGCGATCGGGGACCCACTCTTGTAGTGTGGGCCCTGCTATTTGCGGGGGCATG	5162
Db	5100	TAGTTCGCTGCGACGCTGGGCGCATCTTGTATGATCGGCTAGCTATCGCGGGGGAATG	5159
Qy	5163	ATCTATGCGTCATACACGGGTCTCTCGTGGGTGTTACAGACTGGGATGTCAAGGGGCT	5222
Db	5160	ATCTACGCGTCATACACGGGTGCTGTAGTGTGGGTGACAGACTGGGATGTGAAGGGGCT	5219
Qy	5223	GGCAGCCCCCTTTATCGGCATGGAGCAGGCCACGCCGCCAGCCGGTGTGACAGTCCCC	5282
Db	5220	GGCAGCCCCCTTTATCGCATGGAGACGAGCCAGCCCGCTACGCCGTGGTACAGTTCCT	5279
Qy	5283	CCGTGAGCATCGCCGGGGGAGAGTCTGGCCCATCGGATGCCACACAGTAGACAGAT	5342
Db	5280	CCGTGAGCATCGCCGGGGGTGAATCAGCACCATCGGATGCCACAGAGTAGACAGAT	5339
Qy	5343	CGGTGGCGGCATCCAGGTGGATTGCGATTGGTCAGTCATGACCTGTCGATCGGGAA	5402
Db	5340	CGGTGGCAGCATCCAGGTGGACTGCGATTGGACTATCATGACTCTGTCGATCGGAA	5399
Qy	5403	GTGCTGTCTTGGCCAGGCTTAAGACGGCCGAGGCTTACGCAAGTACACCAAGTGCTT	5462
Db	5400	GTGTTGTCTTGGCTTACGAGCCGAGGCTTACAGCAACGCCAGTGCCTC	5459
Qy	5463	GCTGGCTGTACAGGGGACGGGGCGTCCCACTGTTCAATTGTTGACAGCTCTTC	5522
Db	5460	GCTGGCTGTATACGGGGACGGGGCGTTCACACTGTATCCATTGTTGACAACTCTTC	5519
Qy	5523	GCGGGGCTGGCGCGTGTAGGCCATTGCCACAGTGAATAGCTGGCGAGTGGG	5582
Db	5520	GCGGAGGTTGGCGGCTGTGTGGGCCATTGCCACGCTGATGTCGCGGGGTGGG	5579
Qy	5583	GCCTATGGGCTTCTAGGAGCCCTCATTTGGCTGCTCGGCTTCTACTCATGGGTTG	5642
Db	5580	GCCTACGGGCTTCAAGAGACCGCGTGTGGACCGCGGCTTCTACCTGATGGGTTG	5639
Qy	5643	GGGCTGGAGGCAACCGCCCTTAGCCTCCGCTCTCTACTAGGGGCGGCTGGG	5702
Db	5640	GGGCTGGAGGCAACGCTCAGACGCGCTGGCGTCTGCCCTCTATTGGGGCTGCTGGA	5699
Qy	5703	ACGCTCTGGGACGCTCTGTTGGGTTAACCATGGCGGGCGGTTCATGGGAAGTCT	5762
Db	5700	ACGCTCTGGGACCTCTCTGTTGGGTTGACCATGGCAGGTGGGTTGTTGTTG	5759
Qy	5763	AGGCTCTCCCTCTTGTGTACCAATTTTACTGGGGCGGTGGGGGCTGGGAGGGCTG	5822
Db	5760	AGTGTCTCCCTCTTGTGTACCAATTTTATTTGGGGCGGCTCGGAGGTTGGGAGGGT	5819
Qy	5823	GTGAATGGGCTAGCCCTGCTCTCGACTTATTTGCGGGGAACTATCATCAGAAATCTG	5882

[illegible]

Db 6900 CCTCTCTTTGTGTAGTCCGAGAGATGCTGTATGGGAGAAAGACATCCCCCGTACT 6959
Qy 6963 CCATCGCCAGCACTTATCTCGGTACTGAGAGACGCCAGATGAGAAAGACCCCGTCGTFG 7022
Db 6960 CCATCGCCAGCACTTATCTCGGTACTGAGAGACGCTCAGATGAGAAACCCCGTCGTFG 7019
Qy 7023 TCTTCTCCGAGGAGATACCCCGCTCTCTGACTCATCTCGAGGTGCATCAAGAGTCCGAG 7082
Db 7020 TCTCTCTCGAGGAGATACCCCGCTCTCTGACTCATCTCGAGGTGCATCAAGAGTCCGAG 7079
Qy 7083 ACAGCCGAAGGGAGGAAAGCGTCTCAACGTGGCTCTTTCCGTAATAAGCCCTTGTTT 7142
Db 7080 ACAGCCGAAGGGAGGAAAGTCTCTCAACGTGGCTCTTTCCGTAATAAGCCCTTATTT 7139
Qy 7143 CCACAGCGCATGCCACAGAAGCTTACCGTTAAGATGTGATGCTGTGTTGAGAAGAGC 7202
Db 7140 CCACAGCGCAGCGACCAAGAGCTTACCGTCAAGATGTGCTGCTGTGTTGAAAAGAGC 7199
Qy 7203 GTAACACGCTTCTTTTCATTTGGGATTTGACGCTCGCTGCGTAGCGTCTGTGAGATG 7262
Db 7200 GTCACGCGCTTTTCTCATTTGGGTTGACGCTGGCTGATGTGCTAGCCTGTGTGAGATG 7259
Qy 7263 GAAATCCAGAACCATACAGCCTATTGTGACAAAGTGGCGACTCCGCTTGAATTCGAGTT 7322
Db 7260 GAAATCCAGAACCATACAGCCTATTGTGACCAGGTGCGCACTCCGCTTGAATTCGAGTT 7319
Qy 7323 GGGTCTTTGGTGGGCAATGAACCTTACCTTTGAATGTGACAGTGTGAGGCTAGGCAAGAG 7382
Db 7320 GGGTCTTTGGTGGGCAATGAACCTTACCTTTGAATGTGACAGTGTGAGGCTAGGCAAGAA 7379
Qy 7383 ACCTTGGCTTCTCTTCTTACATTTGGTCTGGGTTGCCACTCACGAGGGCCACTCCGGCC 7442
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Qy 7443 AAGCCCCCTGTGGTGGCGGCTGGCTCTTGTGTTGGTGGCGGACACCAAGTGTAT 7502
Db 7440 AAGCCCTCCGCTGGTGGGCGGCTGGCTCTTGTGTTGGTGGCGGACACTAAGGTTGAT 7499
Qy 7503 GTCACCAACCCGGACAATTTGGGAGAGAGTTGACAAGGTTTACCTCTGGCTGCCCT 7562
Db 7500 GTTACCAATCCAGACAAATGTGGGCGGAGGTTGGACAAGTGTGACCTCTGGCGTCTCT 7559
Qy 7563 AGGGTTATGACAAATTCCTCTGTGACTCCATPAGACGCGCTAAGAGGGCAGCTCAAGCC 7622
Db 7560 AGGGTTATGATAGTACCTCTGTGACTCTATTGAGCGCGCTAAGAGGGCGCTCAAGCC 7619
Qy 7623 TGCTTAACATGGGTTACACTTATGAGAGGCAATAAGGACTGTAAAGCCACATGCTGCC 7682
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Qy 7743 GTCCATGACCGGCTCCAGGAGATCTTGAAGGGAGCGCAGTCCCTTTACTTCTACTGTG 7802
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Qy 7803 AAAAGGAAGTGTCTTCAAGACCGAAGGAAGAGAGAGAGGCCCCCGGCTCATGTGTTC 7862
Db 7800 AAAAGGAAGTGTCTTCAAGACCGAAGGAAGAGAGAGGCCCCCGGCTCATGTGTTC 7859
Qy 7863 CCCCCCTGGACTTCCGATAGCTGAAAGCTTATCTGGGAGACCCCTGGAGGGTAGCC 7922
Db 7860 CCCCCCTGGACTTCCGATAGCTGAAAGCTCATCTTGGGAGACCCAGCGGGTAGCC 7919
Qy 7923 AAGCGGTGTTGGGGGGGCTTACGCCCTTCCAGTACACCCCAATTCAGCAATTAGGAG 7982
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Qy 7983 ATGCTCAACATGTGGGAATCAAGAGACACCATGCGGCCATCTGTGTGAGCGCCACATGC 8042
Db 7980 ATGCTCAAGCTATGGGAGTCTAAGAGAGACCCCTTGGCCATCTGTGTGAGCGCCACCTGC 8039

Qy 8043 TTCGACAGTAGCATAACTGAAGAGACGCTGGCGCTGGAGACAGAGCTTTATGCCCTGGCT 8102
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Qy 8103 TCAGACCATCAGAAATGGGTGCGTCCCTGGGAAATACTATGCTCTGGCACAAATGTA 8162
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Qy 8163 ACCCCGAGGGGTGCCAGTGGGTGAGAGTATTGTAGATCCTCAGGGGTCTTGACCACC 8222
Db 8160 ACCCCGAGGGGTGCCAGTGGGTGAGAGTATTGTAGATCCTCAGGGGTCTTCTAACAACT 8219
Qy 8223 AGTGAGCACTGCTTGTGACTTGTATCAAGGTGAAAGCGCCTGTGAGAGGTGGG 8282
Db 8220 AGCGGACCACTGCTTGAACCTGTACATCAAGGTGAAAGTGCCTGTGAGAGAGTGGG 8279
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Db 8280 CTGAAAAATGCTCCTCCTCATAGCCGCGATGACTGCTTGCATCATATGTGAGCGCA 8339
Qy 8343 GTGTGCGATCCTAGGAGCGCTTTGGGAGAGCCCTGGGAGGCTACGGGTACGCATGCGAG 8402
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Db 8400 CCTCATATCATGATCATATGGACACGCCCTTCTGCTCCACTTGGCTGCTGAGTGC 8459
Qy 8463 AATGAGATGGAAACGCGCATTTCTTCTGACACGAGCTTTTCGGAGGCCCTCCTCGC 8522
Db 8460 AATGAGATGGAAACGCGCATTTCTTCTGACACGAGCTTTCCGGAGCGCGCTCGC 8519
Qy 8523 ATGTGCGAGGTACAGTACCCCAATGGCTTGGCCCATCGGTTACATCTCTCTATACCT 8582
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Qy 8883 GGTGGGCTGAGTGGCTAGGGGCTGTGTGGCCCTCAGGCTCGGCTTCCCTCCG 8942
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Qy 8943 GAGATTGCTGTATCCCGGGGTTTCCCTTCTCCCTTCTATATGGGGGTGGTTCAT 9002
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Qy 9063 ATCTAGCCCTTCTCGGTTGAATTAATTCATCTGTTGGGCAAGGTCCGGTACTGATC 9122
Db 9060 ATCTAGCCCTTCTCGGTTGAATTAATTCATCTGTTGGGCAAGGTCTGGTACTGATC 9119

QY	9123	ATCATCGGAGGAGTTCCCGCCCTCCCGCCCGCCAGGGGTCTCCCGCTGGGTAAAAAGGG	9182
Db	9120	ATCACCAGGAGAGTTCCCGCCCTCCCGCCCGCCAGGGGTCTCCCGCTGGGTAAAAAGGG	9179
QY	9183	CCGGCCTTGGGAGGATGGTGTACTAACCCTTGGCAGGGTCAAGCCCTGATGGTGC	9242
Db	9180	CCGGCCTTGGGAGGATGGTGTACTAACCCTTGGCAGGGTCAAGCCCTGATGGTGC	9239
QY	9243	TAATGACATGCCACTTCGGTGGCGGTGCGTACCTTATAGCGGTAAATCCGTGACTACGGGC	9302
Db	9240	TAATGACATGCCACTTCGGTGGCGGTGCGTACCTTATAGCGGTAAATCCGTGACTACGGGC	9299
QY	9303	TGCTCGACAGCCCTCCCGGATGGGCGACAGTGCATCTGTATCTGAAGGGGTGCACCC	9362
Db	9300	TGCTCGACAGCCCTCCCGGATGGGCGACAGTGCATCTGTATCTGAAGGGGTGCACCC	9359
QY	9363	GGTAAGAGCTGCGCCCAAGGCGGGTTCTACT	9395
Db	9360	GGGAAGAGCTGCGCCCAAGGCGGGTTCTACT	9392
RESULT 12			
AF031827			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
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REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
CDS			

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RESULT 13
AF031828
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DEFINITION Hepatitis G virus strain HGV-1517 polyprotein gene, complete cds.
ACCESSION AF031828
VERSION AF031828.1 GI: 3004902
KEYWORDS
SOURCE
ORGANISM
Hepatitis G virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
GBV-C/HGV group.
1 (bases 1 to 9351)
Bukh,J., Kim,J.P., Govindarajan,S., Appgar,C.L., Fount,S.K.,
Wages,J. Jr., Yun,A.J., Shapiro,M., Emerson,S.U. and Purcell,R.H.
Experimental infection of chimpanzees with hepatitis G virus and
genetic analysis of the virus
J. Infect. Dis. 177 (4), 855-862 (1998)
98194579
PUBMED 9534956
REFERENCE 2 (bases 1 to 9351)
Bukh,J.
Direct Submission
Submitted (29-OCT-1997) Hepatitis Viruses Section, LID, NIAID,
National Institutes of Health, 7 Center Drive 0740, Building 7,
Room 201, Bethesda, MD 20892-0740, USA
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LOCUS	Hepatitis G virus strain HGV-1539 polyprotein gene, complete cds.		
DEFINITION	Hepatitis G virus strain HGV-1539 polyprotein gene, complete cds.		
ACCESSION	AF031829		
VERSION	AF031829.1 GI:3004904		
KEYWORDS	Hepatitis G virus.		
SOURCE	ORGANISM		
REFERENCE	Hepatitis G virus		
	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; GBV-C/HGV group.		
AUTHORS	1 (bases 1 to 9351)		
	Bukh,J., Kim,J.P., Govindarajan,S., Appar,C.L., Fong,S.K., Wages,J. Jr., Yun,A.J., Shapiro,M., Emerson,S.U. and Purcell,R.H.		
TITLE	Experimental infection of chimpanzees with hepatitis G virus and genetic analysis of the virus		
	J. Infect. Dis. 177 (4), 855-862 (1998)		
JOURNAL	98194579		
	MEDLINE		
PUBMED	9534956		
	2 (bases 1 to 9351)		
REFERENCE	Bukh,J.		
	Direct Submission		
AUTHORS	Submitted (29-OCT-1997) Hepatitis Viruses Section, LID, NIAID,		
	National Institutes of Health, 7 Center Drive 0740, Building 7,		
JOURNAL	Room 201, Bethesda, MD 20892-0740, USA		
	Location/Qualifiers		
FEATURES	1. .9351		
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ORIGIN

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Matches 8474; Conservative			90.6%;	Pred. No. 0;	Mismatches 877;	Indels 1;	Gaps		
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ACCESSION AR026878
VERSION AR026878.1 GI:5937718
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9327)
AUTHORS Kim, J. P., Fry, K. E., Young, L. Marie., Linnen, J. M. and Wages, J.
TITLE Hepatitis G virus and molecular cloning thereof
JOURNAL Patent: US 5856134-A 234 05-JAN-1999;
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QY 4240 CAATCATTTAGACAAACTTGACGTGGAGAGATCCCTTCTATGGCATGGCATACCTC 4299
Db 4200 CAATTTAGACAAATTTGACGTGGCGAGATTCCTTTTATGGGCACGGAATACCCC 4259
QY 4300 TTGACGGATGGGACCGGAGGCACTCTGATTCTTGCCACTTCCAAAGCTGAGTCCGAGC 4359
Db 4260 TCGACGGATGGACCGGAGGCACTCTGTTCTGCCATTTAAGCTGAGTCCGAGC 4319
QY 4360 GCGTGGCGGCGAGTTTTCGGGTAGGGGGTTAAATGCCATGCCCTATTACAGGGGGAAG 4419
Db 4320 GCGTTCGTCGCGAGTTCTCCGCTAGGGGGTCAATGCCATTGCCATTATAGGGGTAAG 4379
QY 4420 ACAGTTCTATCAATAAGATGGAGACCTTGGTGGTGTGCTACACAGCGCATATCCACTG 4479
Db 4380 ACAGTTCTATCAATAAGATGGGACCTTGGTGGTGTGCTGCTACAGCGCGCTTTCCACTG 4439

QY 4480 GGTACACTGGGAACCTTCGATTTCTGTCAACGATTTGGTTACTGTGGAGGAGTCTGCTCG 4539
Db 4440 GGTACACTGGAAATTTGACTTCCGTCACCGACTTGGATTAGTGGTGGAGGAGTCTGTG 4499
QY 4540 AGGTGACCCCTTGATCCCACTTACCATCTCCCTCGCACGCTGCGCGCTCGCGTGAAC 4599
Db 4500 AGGTGACCCCTTGATCTTACCATTTACCATCTCCCTCGGACACTGCTGCTCGCTGAC 4559
QY 4600 TGTGATGAGCGGGGAGGACGACCGGATAGGGGAGGTCTGGGCGCTACTACTAGCGGG 4659
Db 4560 TGTGATGCAAGACGAGGACGACCGGATAGGGGAGGTCTGGAGCTACTACTAGCGGG 4619
QY 4660 GGGTCGGAAGGCCCTCTGCTGTGTGTGCTCAGTCTCAGTCTGCTGCTGGCGGGTGAAG 4719
Db 4620 GGGTGGGCAAGGCCCTCGGGGTGTGTGCTCAGTCTCAGTCTGCTGCTGGCGGGTGAAG 4679
QY 4720 CCGGTGTGACCTGTGACGAAATGGAACCTGACCTGACAGCAAACTACTGAGACTTTAG 4779
Db 4680 CTGGAGTGACCTGTGACGAAATGGAACCTGACTTTCACAGCTAACCTACTGAGACTTTAG 4739
QY 4780 ACAACTGCGCTTACACCGGAGCGCTGCGAGCTGACATTTGGGGAAGCGCGGTCTTTT 4839
Db 4740 AGGACTGCGCTTACACCGGAGCGCTGCGGCTGATATCGGAGAAGCGCGGTCTTTCT 4799
QY 4840 CGGGGCTTCCCGCTTGGAGTGCATCCGATTTAGCTGGGCAAAAGTTCCGCGCTCA 4899
Db 4800 CTGGGCTCGCCCATTAGAGTGCACCTGATGTCAGTGGGCAAAAGTTCCGCGGCTCA 4859
QY 4900 ACTGCCCTTCTGCTGGGTGTTACGCGGACCATGTCGCGGGAACACTGCTCCCGGCC 4959
Db 4860 ACTGCCCTTCTGCTGGGTGTTACGCGGACCATGTCGCGGGAACACTGCTCCCGGCC 4919
QY 4960 CATCGGATGACCCCGCTGAGGAGGCTGGAAGGGCCGCAATCCTGTCGCCACTCTCTG 5019
Db 4920 CATCGGATGACCCCGCAATGGGAGGCTGGAAGGGCCCAATCCTGTCGCCACTCTCTG 4979
QY 5020 GGTGGGCAATGATTTACCATCTAAAGTGGCGGCGCATCACATCTGGAAGACCTGGTCC 5079
Db 4980 GGTGGGCAATGATTTACCATCTAAAGTGGCGGCGCACCATAGTGGAGACCTGGTCC 5039
QY 5080 GTAGCTCGGGGTGGCGAGGTTACGTCGCTGCGATGCGGAGCCCATCTTTGATGGTGG 5139
Db 5040 GGAGACTCGGTGTGGCGAGGTTTACGCCGCTGCGAGCTGGCGGATCTTTGATGATCG 5099
QY 5140 GCCTCGCTATTCGCGGGGSCATGATCTATGCTGCTATACACCGGCTCTCTGCTGGTGA 5199
Db 5100 GTCTAGCTATCGCGGGGGAATGATCTAGCGCTGCTACACCGGGTGGCTAGTGGTGA 5159
QY 5200 CAGACTGGGATGTGAAGGGGGTGGCAGCCCTTTATCGGCATGGAGACCGCACGC 5259
Db 5160 CAGACTGGGATGTGAAGGGGGTGGCAGCCCTTTATCGGCATGGAGACCGCACGC 5219
QY 5260 CCCAGCCGGTTGTGAGGTCCCGCGGTAGACCATCGCGCGGGGGAGTCTGGCCAT 5319
Db 5220 CTCAGCCGGTGTGAGGTTCCTCCGGTAGACCATCGCGCGGGGGTGAATCAGCACCAT 5279
QY 5320 CGGATGCCAAACACTGACAGATCGGTGGCGGCATCCAGGTGGATTCGGATTGGTCAG 5379
Db 5280 CGGATGCCAAACACTGACAGATCGGTGGCGGCATCCAGGTGGATTCGGATTGGTCAG 5339
QY 5380 TCATGACCCCTGTGATCGGGGAAGTGTCTCTTGGGCCAGGCTAAGACGGCGCGAGGCT 5439
Db 5340 TCATGACTCTGTGATCGGGAAGTGTGCTCTTGGCTCAGGCTAAGACGGCGCGAGGCT 5399
QY 5440 AGCGAGCTTACCAACAGTGGCTTGTGCTGTCTACACGGGAGCGCGGCGCTCCCACTG 5499
Db 5400 ACACAGCAGCCAGTGGCTGCTGCTGTATACGGGAGCGCGGCGCTTCCCACTG 5459
QY 5500 TTTCAATTGTCACAGCTTTCGCGGGGGCTGGCGGCGGTGGTAGGCCATTCGCCACA 5559
Db 5460 TATCATGTTTGACAAGCTCTTCGCGGGAGGCTGGCGGCTGTGGTGGGCCATTCGCCACA 5519

Qy	5560	GTGTAATAGCTGCGGCAGTGGCGGCTATGCGGCTTCTAGAGAGCCCTCCATTGGCTGCTG	5611
Db	5520	ACGTGATTGCTGCGGCGGTGGCGGCTACGCGGCTCTAAAGAGCCCGCGTTCGACGCG	5579
	5560	CCGCTTCCTACCTCATGCGGTTGGGCGTCGAGGCAACGCGCAACCGGCTTAGCCTCCG	5679
Db	5580	CGGCTTCCTACCTGATGGGTTGGGCGTTGGAGGCAACGCTCAGACGGCTCTGGCATCTG	5639
Qy	5680	CTCTCCTACTAGGGGCGCTGGGACCGCTCTGGGCACGCGCTCTGCTGGGGTTAAACATGG	5739
Db	5640	CCCTCCTATTGGGGGCTGCTGGAAACCGCCTTGGGCACCTCTGCTGGTGGCTTGACCATGG	5699
Qy	5740	CGGCGCGGTTATGCGGAAGTGTGTAGCGTCTCCCGCTCTCTGGTCAACATTTTACTGCGGG	5799
Db	5700	CAGGTGCGTTTCATGGGGGCGCGAGTGTCTCCCGCTCTGGTCAACATTTTATTGGGGG	5759
Qy	5800	CCGTGGGGGCTGGGAGGCGTGGTGAATGCGGCTAGCCTTGTCTTCACATTTTATGGCGG	5859
Db	5760	CCGTCGGAGGTTGGGAGGTTGTTCACGCGCGGAGCGCTAGTCTTTGACTTTCATGGCGG	5819
Qy	5860	GGAACATATCATCAGAAGATCTGTGTTATGCCATCCCACTGAACAGTTCACCGTGGGCGAG	5919
Db	5820	GGAACATTTTCATCAGAAGATCTGTGTTATGCCATCCCGGTACTGACCAACCGCGGGCGG	5879
Qy	5920	GACTTGGCGGGATCGCCCTCGGTTTGGTGTCTACTCAGCTAAACACTCTGGCACTACCA	5979
Db	5880	GCCTTGCGGGGATCGCTCTCGGTTTGGTTTGTATTACCTAACAACTCTGSCACTACCA	5939
Qy	5980	CTTGGTTGAACGTTCTGTGACTACATATGCCAAGTCTCTCATGCATYCCCTGACAGTTACT	6039
Db	5940	CTTGGTTGAACCGTCTGCTGACTACGTTTACCAGGCTTTCATGTATCCCGGACAGTTACT	5999
Qy	6040	TTACAGCAGCGGATTACTGTGCAAGGCTCTCAGCTGTGCTCCGAGCGTTGAGCCTCACTC	6099
Db	6000	TTACAGCAAGTTGACTATGCGGACAGGTTCTACGCGTGCTCCGGCGCTGAGCCTCAACC	6059
Qy	6100	GCACCGTGGTTGCCCTGGTCAACAGAGGAGCCCTAAGGTGGATCAGGTTTCAGCTGGGGTACG	6159
Db	6060	GCACAGTGGTTGCCCTGGTCAACAGAGGAGCCCTAAGTGGATGAGTACAGCTGGGGTATG	6119
Qy	6160	TCTGGGACTTGTGGGAGTGATCGCTCAGTGCGCATGTCGCATGTAAGCCAGACTTCGGG	6219
Db	6120	TCTGGGACTTGTGGGAGTGATCATCGGCCAAGTTCGGGCTGGTCTATGGCCAGACTCAGG	6179
Qy	6220	CCCTCTCCCGTGTCTCATTAACCTTATGCACTCGGGGAGGGGTGTCGCGGAGAT	6279
Db	6180	CCCTCTCCCGTGTGTCTATTACCTTGTGGCATCGGGGAGGGGTGGTCCGGGGAAT	6239
Qy	6280	GGTTGTTGGACGGCCATGTTGAGAGTCGTTGTCTTTGGTTGGCTGATCAACCGGTGATG	6339
Db	6240	GGTTGCTTGACGGTTCATGTTGAGAGTCGCTGCTCTGTGGCTGCGCATCACTGTTGACG	6299
Qy	6340	TTTTGAATGGCAACTCAAGAATCCAGTTTACTTACCAAGCTGTGCAAGCAATTAATGGA	6399
Db	6300	TTCTGAATGGCAACTCAAGAACAGTTTACTTCTACCAAGCTGTGCGGCACTATTGGA	6359
Qy	6400	TGGGACAGTCCCTGTGTGAACATGCTGGGCTATGGCGAGAGCTGCCTTTGCTCCGCTCAG	6459
Db	6360	TGGGACTGTCCCTGTGAACATGCTGGGTTACGGTGAACAGTCGCGCTCTCTGGCCTCCG	6419
Qy	6460	ACACCCGAAGTGTACCATTTTCGGGACGCTCTGGGTGGGCTCAGGTGTGTGACCCCTA	6519
Db	6420	ACACCCGAAGTGTGCCCTTCGGGACGCTCTGGCTGGGCTGAGTGTGTGACCACTA	6479
Qy	6520	CCACGTTGTGATCAGGCAACATCCGCGCTCAACAACTGCTGGCGCAGCAAAATCTGTGCG	6579
Db	6480	CCACGTTGGTAATCAGGAGAACTCCGCGCTATAAGCTGCTGCGCAGCAAAATCTGTGCG	6539
Qy	6580	CTGCTGTGTCTGAGCCCTATTAGTCGACGGCATACCGGCTCTCATGGACCGCACGCGC	6639
Db	6540	CTGCTGTAGCTGAGCCCTACTAGCTCGACGGCATTCGCGCTCTCATGGACCGCACGCTC	6599
Qy	6640	GAGCGCTGCCATGGTCTATGCGCCTTGGGCAAGTGTCAACATTTGACGGGGAAGGCTACA	6699

[illegible]

Db 7680 CCACCCCGCGGGAAGATGGCCGCTCCATGACCGGCTCAGGAGATACTTGAAGGACTC 7739
QY 7780 CAGTCCCTTACTCTTACTGTGAAGAGAGTCTTCTCAAGACCGAAGAGAGAGA 7839
Db 7740 CCGTCCCTTACTCTTACTGTGAAGAGAGTCTTCTCAAGACCGAAGAGAGAGG 7799
QY 7840 AGGCCCCCGGCTCATTTGTGTCCCGCTTGGAGTTCGGATAGCTGAAAGCTTATTC 7899
Db 7800 AGGCCCCCGGCTCATTTGTGTCCCGCTTGGAGTTCGGATAGCTGAAAGCTCATCT 7859
QY 7900 TGGGAGACCTTGGAGGCTAGCAAGGCGGTGTGGGGGGGCGCTACGCCCTTCCAGTACA 7959
Db 7860 TGGGAGACCTTGGAGGCTAGCAAGGCGGTGTGGGGGGGCGCTACGCCCTTCCAGTACA 7919
QY 7960 CCCCAGGCTAGGAGATGCTCAAACTGTGGGAATCAAGAGACACCATCGG 8019
Db 7920 CCCCAGGCTAGGAGATGCTCAAACTGTGGGAATCAAGAGACACCATCGG 7979
QY 8020 CATCTGTGTGGACGCCACATGCTTCGACAGTAGCATAACTGAAGAGACGTTGGCGTGG 8079
Db 7980 CCATCTGTGTGGACGCCACCTGCTTCGACAGTAGCATAACTGAAGAGACGTTGGCGTGG 8039
QY 8080 AGACAGACCTTATGCCCTTGGCTTCAGACCATCCAGATGGGTGGCGCTGCCCTGGGGAAT 8139
Db 8040 AGACAGACCTTATGCCCTTGGCTTCAGACCATCCAGATGGGTGGCGCGCACTTGGGGAAT 8099
QY 8140 ACTATGCTGTGGCAACAATGTTAAACCCCGAGGGGTGCCAGTGGGTGAGAGGTATTGTA 8199
Db 8100 ACTATGCTGTGGCAACAATGTTAAACCCCGAGGGGTGCCAGTGGGTGAGAGGTATTGTA 8159
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Db 8160 GATCTCAGGGTCTTGAACCACTGCGAGCAACTGCTTGACTTGTCTATATCAAGGTGA 8219
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QY 8380 CGAGCTACGGGTACGATCGGAGCCTTCGTATCATGATCATGACACGCGCCCTTCT 8439
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QY 8500 ACTTTCGAGGCGCCTCGCTGCGATGCTGAGGAGTACAGTACACCAATGGCTTCGGCCA 8559
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QY 8620 TGCTCACCTGGCGTTTAGGGGTGGTGGCACACCGCTGTGATCTGTGGTGCCAGGTAC 8679
Db 8580 TGCTAACGTGGGCATTCAGGGGTGGAGGACACACCGCTGTGATCCGGTTTGGTGCCAGGTAC 8639
QY 8680 ATGGTAATTAATACAGTTCACCTGGACAACTGCCTTAACATCATCGTGGCCCTCCACG 8739
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QY 8800 TGCTGAGGAGCTCAAGCTCCCTGGCTAGCAGTCCACCGGAAGAGCCGGGGCATTTGC 8859
Db 8760 TTCTGAGGAGCTCAAGCTCCCTGGCTAGCAGTCCACCGGAAGAGCCGGGGCGTTGC 8819

QY 8860 GAACCGCTATGCTCCGCTCGCGCTTGGGCTGAGTGGCTAGGGGCTGTTTGTGGCGTC 8919
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QY 8980 CCCCCTATATGGGGTGGTTTCATCAATTTGGATTTCACAAGCCAGAGAGTCCGTCGCGGT 9039
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QY 9040 GGTTCGGGTTCCTTAGCCCTGCTCATCGTAGCCCTCTTTCGGGTGAACCTAAATTCATCTGT 9099
Db 9000 GGTTCGGGTTCCTTAGCCCTGCTCATCGTAGCCCTCTTTCGGGTGAACCTAAATTCATCTGT 9059
QY 9100 GCGGCAAGTCCGGTACTGATCATCTAGGAGGTTTCCCGCTTCCCGCCCGCCAGGG 9159
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Db 9120 GTCTCCCGCTGGGTAAAAGGGCCCGCTTGGGAGGATGGTGTACTAAACCCCTG 9179
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Db 9240 TAGCCTAATCCGTGACTACGGGCTCTCGCAGAGCCCTTCCCGGATGGGGCACAGTGCAC 9299
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Db 9300 TGTGATCTGAAGGGGTGCACCCCGGTA 9327

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